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(57) Abstract			
<p>Polypeptides possessing a novel activity, namely endo-xylogalacturonase activity, are disclosed. These polypeptides can degrade pectin found in plant extracts and plant materials, and in particular the "hairy" regions of pectin polymers. In particular, the polypeptides can cleave in a galacturonic acid polymer at internal glycosidic bonds. The novel enzyme XghA is disclosed, and its amino acid sequence and encoding DNA sequence given. This polypeptide was expressed in yeast cells and has been used to treat vegetable material, in particular soy and fruit juice in the preparation of edible foodstuffs.</p>			

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NOVEL ENDO-XYLOGALACTURONASE

Field of the Invention

The present invention relates to a novel endo-xylogalacturonase (XGH) and homologues thereof. It further relates to the use of the endo-xylogalacturonase in a method
5 of processing plant or pectin-containing material to produce fruit juice and other plant extracts.

Background to the Invention

Enzyme preparations are often used during the processing of plant materials, for example in the steps of extraction and liquefaction of fruit and fruit juice and their filtration
10 and clarification. Commercial enzyme preparations contain a mixture of enzymes which degrade the pectin polymers which are a major component of plant cell walls. Such enzymes include pectin lyases, polygalacturonases, pectin esterases, celluloses, xyloglucanases, galactanases and arabinanases.

Pectins occur in nature as constituents of higher plant cell walls. They are found in
15 primary cell wall lamella where they are embedded in between the cellulose fibrils. The composition of pectin is variable among plant species and moreover dependent on the age and the maturity of the fruit. Among the richer sources of pectins are lemons and oranges, which can represent up to 30% of polysaccharides present.

Most pectin polymers are comprised of 'smooth' homogalacturonan regions and
20 ramified 'hairy' regions. The 'smooth' regions consist of a linear homogalacturonan backbone. The 'hairy' regions of apples consists of three different subunits: subunit I is xylogalacturonan (a galacturonan backbone heavily substituted with xylose); subunit II is a short section of a rhamnogalacturonan backbone, rich in relatively long arabinan, galactan and/or arabinogalactan side chains (the 'hairs'); and subunit III is a rhamnogalacturonan
25 oligomer, having a backbone consisting of an alternating sequence of rhamnose and galacturonic acid residues.

Many of the well-known pectinases used in industrial food processing degrade only the 'smooth' part of the pectin polymer leaving the 'hairy' regions intact. Consequently, during for example apple juice production, the non-degraded parts of the pectin polymer cause production losses due to inefficient filtration as a result of fouling of the
5 (ultra)filtration membrane.

Several enzymes have been reported which can degrade parts of the 'hairy' region, for example the rhamnogalacturonan regions of the backbone (subunit III). These enzymes are referred to as rhamnogalacturonases (RGases), of which there are several types. However, so far the xylogalacturonan part of the 'hairy' regions (subunit I) has been resistant to
10 enzymatic digestion and so in prior art enzymatic endo-digestion processes the xylogalacturonan is left as an inert carbohydrate.

Since xylogalacturonan has also been found in many other plants, e.g. leguminous plants like soybeans and peas, watermelons, grapes and pine pollen, enzymes to degrade this polymer would be useful for the processing of plant material.

15 An exo-galacturonase (42kDa, SDS-PAGE) has been identified¹ that is not hindered by the single unit xylose side-chains and is able to degrade xylogalacturonan using a soluble 'hairy' pectic polysaccharide from soy as substrate. This enzyme acts in an exo-fashion as it yields galacturonic acid or a disaccharide consisting of galacturonic acid and xylose. The enzyme was purified to near homogeneity (Fractions HTP2 and Q2) and
20 partially characterized. By contrast to known RGases (which do not degrade homogalacturonic acid) this enzyme is not very specific for xylogalacturonan as it also acts on pectic acid. In addition, this enzyme is not able to digest the xylogalacturonan backbone in a random fashion, and therefore to date there are no known enzymes possessing endo-xylogalacturonase activity.

25

Disclosure of the Invention

The present invention has resulted from the isolation and characterization of a novel endo-xylogalacturonase and cDNA encoding it. The endo-xylogalacturonase cDNA sequence is set out in SEQ. ID No. 1. The amino acid sequence of the ORF from nucleotides 98 to 1315 is set out in SEQ. ID No. 2.

30 In a first aspect of the invention there is provided an (e.g. isolated and/or purified)

polypeptide possessing endo-xylogalacturonase activity. There is also provided a polypeptide comprising an endo-xylogalacturonase, such as a polypeptide comprising the sequence set out in SEQ ID No. 2, or a polypeptide substantially homologous thereto, or a fragment of the polypeptide of SEQ ID No. 2 having at least 5 amino acids.

5 The polypeptide of the invention preferably has one or more of the following additional features, namely it:

- (1) possesses endo-xylogalacturonase activity;
- (2) has an optimal pH-range of from 2.5 to 6;
- (3) has optimum activity at a temperature of from 50 to 70°C; and/or
- 10 (4) has a molecular weight (deglycosylated) of from 40 to 50 kDa.

"Endo-xylogalacturonase activity" is defined as the ability to cleave a galacturonic acid polymer (for example as found in pectin) which may be at least partially substituted with xylose at internal glycosidic bonds. The activity thus allows cleavage between adjacent galacturonan non-terminal units (where neither of such units is at the end of the polymer, which is in contrast to exo activity where the end unit would be cleaved).
15 Preferably the cleavage occurs at a [galacturonic acid (1-4) galacturonic acid] linkage. Preferably, the polypeptide does not cleave terminal xylose residues from xylose substituted galacturonic acid residues, for example a [galacturonic acid (3-1) xylose] linkage. The polypeptide may preferentially cleave in between two adjacent non-xylose substituted galacturonan units. The substrate polymer may be from 40 to 80% (e.g. xylose) substituted.
20

The two galacturonic acid residues between which the polypeptides of the invention cleave may both be (xylose) substituted, or only one may be (xylose) substituted or (preferably) neither may be (xylose) substituted. Alternatively or in addition the two
25 galacturonic acid residues may both be methylated, or one may be methylated, or (preferably) neither may be methylated.

Preferably, the polypeptide of the invention is obtainable from a microorganism which possesses a gene encoding an enzyme with endo-xylogalacturonase activity. More preferably the microorganism is a microbial organism, preferably fungal, and optimally a
30 filamentous fungi. Preferred organisms are thus of the genera *Aspergillus*, *Trichoderma*, *Penicillium*, *Acremonium*, *Fusarium*, *Humicola*, *Neurospora*, *Mucor*, *Scytallidium*, *Myceliophthora*, *Thielavia*, *Talaromyces*, *Thermomyces*, *Thermoascus*, *Chaetomium*,

Sporotrichum, *Corynascus*, *Calcarisporiella* or *Mycelia*. Optionally the organism is of the species from the *Aspergillus niger* group (as defined by Raper and Fennell, The Genus *Aspergillus*, The Williams & Wilkins Company, Baltimore, pp 293-344, 1965), specifically including but not limited to *Aspergillus niger*, *Aspergillus awamori*,
5 *Aspergillus tubigensis*, *Aspergillus aculeatus*, *Aspergillus foetidus*, *Aspergillus japonicus* or *Aspergillus ficuum*.

In a second aspect, the present invention provides an (e.g. isolated and/or purified) polynucleotide encoding a polypeptide of the first aspect of the invention. For example the present invention provides a polynucleotide encoding an endo-xylogalacturonase, such an
10 endo-xylogalacturonase whose amino acid sequence is set out in SEQ ID No. 2. The present invention further provides a polynucleotide encoding a polypeptide having substantial amino acid sequence homology to the amino acid sequence set out in SEQ ID No. 2. Also provided is a polynucleotide selected from:

- 15 (a) polynucleotides comprising the nucleotide sequence set out in SEQ ID No. 1, or the complement thereof;
- (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequence set out in SEQ ID No. 1, or a fragment thereof;
- (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequence set out in SEQ ID No. 1, or a fragment
20 thereof; and/or
- (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

A polynucleotide of the invention also includes a polynucleotide which:

- a. encodes a polypeptide having endo-xylogalacturonase activity, which
25 polynucleotide is:

- (1) the coding sequence of SEQ ID No. 1;
- (2) a sequence which hybridises selectively to the complement of sequence defined in (1); or
- (3) a sequence that is degenerate as a result of the genetic code with respect to a
30 sequence defined in (1) or (2); or
- b. is a sequence complementary to a polynucleotide defined in (a).

The term "capable of hybridizing" means that the target polynucleotide of the

invention can hybridize to the nucleic acid used as a probe (for example the nucleotide sequence set out in SEQ. ID No.1, or a fragment thereof or the complement thereof) at a level significantly above background. The background hybridization may occur because of, for example, other polynucleotides, such as DNA, present in, for example a
5 cDNA/genomic library being screened. In this event, background implies a level of signal generated by interaction between the probe and a non-specific polynucleotide member of the library which is less than 10 fold, preferably less than 100 fold, as intense as the specific interaction observed with the target polynucleotide. The intensity of interaction may be measured, for example, by radiolabelling the probe, e.g. with ^{32}P . Suitable
10 conditions are described later.

Preferably, the polynucleotide of the invention is obtainable from the same organism as the polypeptide, such as a fungus, in particular a fungus of the genus *Aspergillus*.

The present invention also provides a polynucleotide probe which comprises a fragment of at least 15 nucleotides of a polynucleotide of the invention as described above.

15 In a third aspect, the invention provides vectors comprising a polynucleotide of the invention, including cloning and expression vectors, and in a fourth aspect methods of growing, transforming or transfecting such vectors in a suitable host cell, for example under conditions in which expression of a polypeptide of, or encoded by a sequence of, the invention occurs. Provided in a fifth aspect are host cells comprising a polynucleotide or
20 vector of the invention wherein the polynucleotide is heterologous to the genome of the host cell. The term "heterologous to the genome of the host cell" means that the polynucleotide does not naturally occur in the genome of the host cell. Preferably, the host cell is a yeast cell, for example a yeast cell of the genus *Kluyveromyces* or *Saccharomyces* or a fungal cell, for example of the genus *Aspergillus*.

25 The polypeptides of the invention which possess endo-xylogalacturonase activity may be used in a sixth aspect to treat plant material including plant pulp and plant extracts. For example, they may be used to treat apple pulp and/or raw juice during the production of apple juice. Conveniently the polypeptide of the invention is combined with suitable carriers or diluents including buffers to produce a composition/ enzyme preparation. Thus
30 the present invention provides in a seventh aspect a composition comprising a polypeptide of the invention. The composition may further comprise additional ingredients such as one or more enzymes, for example pectinases, including endo-arabinanase and

rhamnogalacturonase, cellulases and/or xyloglucanases.

The polypeptides and compositions of the invention may therefore be used in a method of processing plant material to degrade or modify the pectin constituents of the cell walls of the plant material. Thus in an eighth aspect, the present invention provides a method of degrading or modifying a plant cell wall which method comprises contacting the plant cell wall with a polypeptide or composition of the invention.

The invention also provides a method of processing a plant material which method comprises contacting the plant material with a polypeptide or composition of the invention to degrade or modify the pectin in the plant material. Preferably the plant material is a plant pulp or plant extract.

In particular, the degradation preferably comprises endo-type cleaving of xylogalacturonan subunits of a pectin component of the plant cell wall. The plant material is preferably a fruit or vegetable pulp or fruit or vegetable extract, for example apple pulp or apple juice.

The present invention further provides a processed plant material obtainable by contacting a plant material with a polypeptide or composition of the invention. Preferably the processed plant material is a fruit or vegetable juice, for example apple juice.

The present invention also provides a method for reducing the viscosity of a plant extract which method comprises contacting the plant extract with a polypeptide or composition of the invention in an amount effective in degrading pectins contained in said plant extract.

Preferred features and characteristics of one aspect of the invention are applicable to another aspect *mutatis mutandis*.

Detailed description of the invention

25 A. Polynucleotides.

The invention provides a polynucleotide which:

a. encodes a polypeptide that has endo-xylogalacturonase activity, which polynucleotide is:

(1) the coding sequence of SEQ ID No. 1;

30 (2) a sequence that hybridizes selectively to the complement of the sequence

defined in (1); or

(3) a sequence that is degenerate as a result of the genetic code with respect to the nucleic acid sequence defined in (1) or (2); or

b. is a sequence complementary to a polynucleotide defined in (a).

5 The polynucleotides of the invention also include variants of the coding sequence of SEQ ID No. 1 which have endo-xylogalacturonase activity. Variants may be formed by additions, substitutions and/or deletions. Such variants may thus have the ability to cleave internally a galacturonic acid polymer. Typically a polynucleotide of the invention comprises a continuous sequence of nucleotides which is capable of hybridizing under
10 selective conditions to the complement of the coding sequence of SEQ ID No. 1.

A polynucleotide of the invention and complement of the coding sequence of SEQ ID No. 1 can hybridize at a level significantly above background. Background hybridization may occur, for example, because of other cDNA's present in a cDNA library. The signal level generated by the interaction between a polynucleotide of the invention and the
15 complement of the coding sequence of SEQ ID No. 1 is typically at least 10-fold, preferably at least 100-fold, as intense as interactions between other polynucleotides and the coding sequence of SEQ ID No. 1. The intensity of interaction may be measured, for example, by radiolabelling the probe, for example with ^{32}P . Selective hybridization may typically be achieved using conditions of low stringency (for example, 0.03M sodium
20 chloride and 0.03M sodium citrate at about 40°C), medium stringency (for example, 0.03M sodium chloride and 0.03M sodium citrate at about 50°C) or high stringency (for example, 0.03M sodium chloride and 0.03M sodium citrate at about 60°C).

A preferred polynucleotide is capable of selectively hybridizing to complement the DNA sequence of SEQ ID No. 1 will generally have at least 50%, at least 60%, at least
25 70%, at least 80%, at least 90%, at least 95%, at least 98% or at least 99% sequence identity to the coding sequence of SEQ ID No. 1 over a region of at least 20, preferably at least 30, for instance at least 40, at least 60, or preferably at least 100 continuous nucleotides or most preferably over the full length of SEQ ID No. 1.

Any combination of the above mentioned degrees of sequence identity and minimum
30 sizes may be used to define polynucleotides of the invention, with the more stringent combinations (that is to say higher sequence identity over longer lengths) being preferred. Thus, for example, a polynucleotide which has least 90% sequence identity over 25,

preferably over 30 nucleotides, is preferred, as is a polynucleotide which has at least 95% sequence identity over 40 nucleotides.

The coding sequence of SEQ ID No. 1 may be modified by nucleotide substitutions, for example from 1, 2 or 3 to 10, 25, 50 or 100 substitutions. The polynucleotide of SEQ ID No. 1 may alternatively or additionally be modified by one or more insertions and/or deletions (such as the same number mentioned for substitutions) and/or by an extension to either or both ends. The modified polynucleotide in general encodes a polypeptide which has endo-xylogalacturonase activity. Degenerate substitution may be made and/or substitutions may be made which would result in a conservative amino acid substitution when the modified sequence is translated, for example as shown in the Table on page 12 in the section concerning polypeptides.

Polynucleotides of the invention may comprise DNA or RNA. They may be single or double stranded. They may also be polynucleotides which include within them synthetic or modified nucleotides. A number of different types of modifications to polynucleotides are known in the art. These include a methylphosphonate and phosphorothioate backbones, and addition of acridine or polylysine chains at the 3' and/or 5' ends of the molecule. For the purposes of the present invention, it is to be understood that the polynucleotides described herein may be modified by any method available in the art.

It is to be understood that skilled persons may, using routine techniques, make nucleotide substitutions that do not affect the polypeptide sequence encoded by the polynucleotides of the invention to reflect the codon usage of any particular host organism in which the polypeptides of the invention are to be expressed.

Polynucleotides of the invention may be used as a primer, e.g. a PCR primer, a primer for an alternative amplification reaction, a probe e.g. labelled with a revealing label by conventional means using radioactive or non-radioactive labels, or the polynucleotides may be cloned into vectors.

Such primers, probes and other fragments will be at least 15, preferably at least 20, for example at least 25, 30 or 40 nucleotides in length. There will typically be up to 40, 50, 60, 70, 100 or 150 nucleotides in length. Probes and fragments can be longer than 150 nucleotides in length, for example up to 200, 300, 400, 500, 600, 700 nucleotides in length, or even up to a few nucleotides (such as 5 or 10 nucleotides) short of the coding sequence of SEQ ID No. 1.

Polynucleotides such as a DNA polynucleotide and primers according to the invention may be produced recombinantly, synthetically, or by any means available to those of skill in the art. They may also be cloned by standard techniques. The polynucleotides are typically provided in isolated and/or purified form.

5 In general, primers will be produced by synthetic means, involving a step-wise manufacture of the desired nucleic acid sequence one nucleotide at a time. Techniques for accomplishing this using automated techniques are readily available in the art.

Longer polynucleotides will generally be produced using recombinant means, for example using a PCR (polymerase chain reaction) cloning techniques. This will involve
10 making a pair of primers (e.g. of about 15-30 nucleotides) to a region of the endo-xylogalacturonase gene which it is desired to clone, bringing the primers into contact with mRNA or cDNA obtained from a fungal, yeast, bacterial plant or prokaryotic cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified fragment (e.g. by purifying the reaction
15 mixture on an agarose gel) and recovering the amplified DNA. The primers may be designed to contain suitable restriction enzyme recognition sites so that the amplified DNA can be cloned into a suitable cloning vector.

Such techniques may be used to obtain all or part of the endo-xylogalacturonase sequence described herein. Genomic clones corresponding to the cDNA of SEQ ID No. 1
20 or the endo-xylogalacturonase gene containing, for example, introns and promoter regions are within the invention also and may also be obtained in an analogous manner (e.g. recombinant means, PCR, cloning techniques), starting with genomic DNA from a fungal, yeast, bacterial plant or prokaryotic cell.

Although in general the techniques mentioned herein are well known in the art,
25 reference may be made in particular to Sambrook *et al.*, Molecular Cloning, A Laboratory Manual (1989) and Ausubel *et al.*, Current Protocols in Molecular Biology (1995), John Wiley & Sons, Inc.

Polynucleotides which do not have 100% identity with SEQ ID No. 1 but fall within the scope of the invention can be obtained in a number of ways. Thus variants of the
30 endo-xylogalacturonase sequence described herein may be obtained for example by probing genomic DNA libraries made from a range of organisms, for example those discussed as sources of the polypeptides of the invention. In addition, other fungal, plant

or prokaryotic homologues of endo-xylogalacturonase may be obtained and such homologues and fragments thereof in general will be capable of hybridising to SEQ ID No.

1. Such sequences may be obtained by probing cDNA libraries or genomic DNA libraries from other species, and probing such libraries with probes comprising all or part of SEQ
5 ID. 1 under conditions of medium to high stringency (for example 0.03M sodium chloride and 0.03M sodium citrate at from 50°C to 60°C). Nucleic acid probes comprising all or part of SEQ ID No. 1 may be used to probe cDNA libraries from other species, such as those described as sources for the polypeptides of the invention.

Species homologues may also be obtained using degenerate PCR which will use
10 primers designed to target sequences within the variants and homologues encoding conserved amino acid sequences. The primers will contain one or more degenerate positions and will be used at stringency conditions lower than those used for cloning sequences with single sequence primers against known sequences.

Alternatively, such polynucleotides may be obtained by site directed mutagenesis of
15 the endo-xylogalacturonase sequences or variants thereof. This may be useful where for example silent codon changes are required to sequences to optimise codon preferences for a particular host cell in which the polynucleotide sequences are being expressed. Other sequence changes may be desired in order to introduce restriction enzyme recognition sites, or to alter the property or function of the polypeptides encoded by the polynucleotides.

20 The invention includes double stranded polynucleotides comprising a polynucleotide of the invention and its complement.

Polynucleotides or primers of the invention may carry a revealing label. Suitable labels include radioisotopes such as ³²P or ³⁵S, enzyme labels, or other protein labels such as biotin and DIG-hapten. Such labels may be added to polynucleotides or primers of the
25 invention and may be detected using by techniques known *per se*.

The present invention also provides polynucleotides encoding the polypeptides of the invention described below. Since such polynucleotides will be useful as sequences for recombinant production of polypeptides of the invention, it is not necessary for them to be capable of hybridising to the sequence of SEQ ID No. 1, although this will generally be
30 desirable. Otherwise, such polynucleotides may be labelled, used, and made as described above if desired.

B. Polypeptides.

A polypeptide of the invention comprises the amino acid sequence set out in SEQ ID No. 2 or a substantially homologous sequence, or a fragment of either sequence and can have endo-xylogalacturonase activity. In general, the naturally occurring amino acid
5 sequence shown in SEQ ID No. 2 is preferred.

In particular, the polypeptide of the invention may comprise:

- a. the polypeptide sequence of SEQ ID No. 2;
- b. a naturally occurring variant or species homologue thereof, or
- c. a protein with at least 60, at least 70, at least 80, at least 90, at least 95, at least
10 98 or at least 99% sequence identity to (a) or (b).

A variant will be one that occurs naturally, for example in fungal, bacteria, yeast or plant cells and which can function in a substantially similar manner to the protein of SEQ ID No. 2, for example it has endo-xylogalacturonase activity. Similarly a species
homologue of the protein will be the equivalent protein which occurs naturally in another
15 species and which can function as an endo-xylogalacturonase enzyme.

Variants and species homology can be obtained by following the procedures described herein for the production of the polypeptide of SEQ ID No. 2 and performing such procedures on a suitable cell source, for example a bacterial, yeast, fungal or plant cell. It will also be possible to use a probe as defined above to probe libraries made from yeast,
20 bacterial, fungal or plant cells in order to obtain clones including the variants or species homology. The clones can be manipulated by conventional techniques to generate a polypeptide of the invention which can then be produced by recombinant or synthetic techniques known *per se*.

The polypeptide of the invention preferably has at least 60% sequence identity to the
25 protein of SEQ ID No. 2, more preferably at least 70%, at least 80%, at least 90%, at least 95%, at least 97% or at least 99% sequence identity thereto over a region of at least 20, preferably at least 30, for instance at least 40, at least 60, at least 100, 200 or 300 contiguous amino acids or over the full length of SEQ ID No. 2.

The sequence of the polypeptide of SEQ ID No. 2 and of variants and species
30 homologues can thus be modified to provide polypeptides of the invention. Amino acid substitutions may be made, for example from 1, 2 or 3 to 10, 20 to 30 substitutions. The

same number of deletions and insertions may also be made. The modified polypeptide generally retains activity as an endo-xylogalacturonase.

Conserved substitutions may be made according to the following Table, where amino acids in the same block in the second column and preferably in the same line in the third column may be substituted for each other:

ALIPHATIC	Non-polar	G A P
		I L V
	Polar - uncharged	C S T M
		N Q
	Polar - charged	D E
		K R
AROMATIC		H F W Y
OTHER		N Q D E

Polypeptides of the invention also include fragments of the above mentioned full length polypeptides and of variants thereof, including fragments of the sequence set out in SEQ ID No. 2. Such fragments typically retain activity as an endo-xylogalacturonase. Fragments may be at least 10, 15, 20, 30, 50, 100 or 200 amino acids long.

Polypeptides of the invention may be in a substantially isolated form. It will be understood that the polypeptide may be mixed with carriers or diluents which will not interfere with the intended purpose of the polypeptide and still be regarded as substantially isolated. A polypeptide of the invention may also be in a substantially purified form, in which case it will generally comprise the polypeptide in a preparation in which more than 50%, e.g. more than 80%, 90%, 95%, 98% or 99% by weight of the polypeptide in the preparation is a polypeptide of the invention. Polypeptides of the invention may be chemically modified, for example post-transnationally modified. For example, they may be glycosylated (one or more times) or comprise one or more modified amino acid residues.

They may be modified for example by the addition of histidine residues or a T7 tag to assist their identification or purification or by the addition of a signal sequence to promote their secretion from a cell, as discussed below.

Polypeptides of the invention can if necessary be produced by synthetic means although usually they will be made recombinantly as described below.

Particularly preferred polypeptides of the invention include a polypeptide consisting of amino acids 19 to 406 of the amino acid sequence set out in SEQ. ID No. 2 since this lacks the N-terminal signal peptide which consists of amino acids 1 to 18 of the amino acid sequence of SEQ ID No. 2. The polypeptides and fragments thereof may contain amino acid alterations as defined above.

The use of yeast and fungal host cells is expected to provide for such post-translational modifications (e.g. proteolytic processing, myristilation, glycosylation, truncation, and tyrosine, serine or threonine phosphorylation) as may be needed to confer optimal biological activity on recombinant expression products of the invention.

10 C. Recombinant Aspects.

Polynucleotides of the invention can be incorporated into a recombinant replicable vector, for example a cloning or expression vector. The vector may be used to replicate the nucleic acid in a compatible host cell. Thus in a further embodiment, the invention provides a method of making polynucleotides of the invention by introducing a polynucleotide of the invention into a replicable vector, introducing the vector into a compatible host cell, and growing the host cell under conditions which bring about replication of the vector. The vector may be recovered from the host cell. Suitable host cells are described below in connection with expression vectors.

Expression Vectors

Preferably, a polynucleotide of the invention in a vector is operably linked to a regulatory sequence which is capable of providing for the expression of the coding sequence by the host cell, i.e. the vector is an expression vector. The term "operably linked" refers to a juxtaposition wherein the components described are in a relationship permitting them to function in their intended manner. A regulatory sequence such as a promoter, enhancer or other expression regulation signal "operably linked" to a coding sequence is positioned in such a way that expression of the coding sequence is achieved under condition compatible with the control sequences.

The vectors may be for example, plasmid, virus or phage vectors provided with an origin of replication, optionally a promoter for the expression of the polynucleotide and optionally a regulation of the promoter.

The DNA sequence encoding the polypeptide is preferably introduced into a suitable host as part of an expression construct in which the DNA sequence is operably linked to expression signals which are capable of directing expression of the DNA sequence in the host cells. For transformation of the suitable host with the expression construct

5 transformation procedures are available which are well known to the skilled person^{3,4}. The expression construct can be used for transformation of the host as part of a vector carrying a selectable marker, or the expression construct is co-transformed as a separate molecule together with the vector carrying a selectable marker. The vectors may contain one or more selectable marker genes.

10 Preferred selectable markers^{3,4} include but are not limited to e.g. versatile marker genes that can be used for transformation of most filamentous fungi and yeasts such as acetamidase genes or cDNAs (the *amdS* genes or cDNAs from *A.nidulans*, *A.oryzae*, or *A.niger*), or genes providing resistance to antibiotics like G418, hygromycin, phleomycin or benomyl resistance (*benA*). Alternatively, more specific selection markers can be used
15 such as auxotrophic markers which require corresponding mutant host strains: e.g. *URA3* (from *S.cerevisiae* or analogous genes from other yeasts), *pyrG* (from *A.nidulans* or *A.niger*) or *argB* (from *A.nidulans* or *A.niger*). In a more preferred embodiment, the selection marker is deleted from the transformed host cell after introduction of the expression construct in accordance with the methods described in EP-A-0 635 574, so as to
20 obtain transformed host cells capable of producing the polypeptide which are free of selection marker genes.

Other markers include ATP synthetase, subunit 9 (*oliC*), orotidine-5'-phosphate-decarboxylase (*pvrA*), the bacterial G418 resistance gene (this may also be used in yeast, but not in fungi), the ampicillin resistance gene (*E. coli*), the neomycin resistance gene
25 (*Bacillus*) and the *E. coli uidA* gene, coding for β -glucuronidase (GUS). Vectors may be used *in vitro*, for example for the production of RNA or used to transfect or transform a host cell.

For most filamentous fungi and yeast, the expression construct is preferably integrated in the genome of the host cell in order to obtain stable transformants. However, for certain
30 yeasts also suitable episomal vector systems are available into which the expression construct can be incorporated for stable and high level expression, examples thereof include vectors derived from the 2 μ and pKD1 plasmids of *Saccharomyces* and



Kluyveromyces, respectively. In case the expression constructs are integrated in the host cells genome, the constructs are either integrated at random loci in the genome, or at predetermined target loci using homologous recombination, in which case the target loci preferably comprise a highly expressed gene. A highly expressed gene is herein defined as
5 a gene whose mRNA can make up at least 0.05% (w/w) of the total cellular mRNA, e.g. under induced conditions, or alternatively, a gene whose gene product can make up at least 1% (w/w) of the total cellular protein, or, in case of a secreted gene product, can be secreted to a level of at least 0.1 g/l. A number of examples of suitable highly expressed genes is provided herein below.

10 An expression construct for a given host cell will usually contain the following elements operably linked to each other in a consecutive order from the 5'-end to 3'-end relative to the coding strand of the sequence encoding the polypeptide of the first aspect: (1) a promoter sequence capable of directing transcription of the DNA sequence encoding the polypeptide in the given host cell, (2) optionally, a signal sequence capable of
15 directing secretion of the polypeptide from the given host cell into the culture medium, (3) the DNA sequence encoding a mature and preferably active form of the polypeptide, and preferably also (4) a transcription termination region (terminator) capable of terminating transcription downstream of the DNA sequence encoding the polypeptide.

Enhanced expression of the polynucleotide encoding the polypeptide of the invention
20 may also be achieved by the selection of heterologous regulatory regions, e.g. promoter, secretion leader and terminator regions, which serve to increase expression and, if desired, secretion levels of the protein of interest from the chosen expression host and/or to provide for the inducible control of the expression of the polypeptide of the invention.

Aside from the promoter native to the gene encoding the polypeptide of the invention,
25 other promoters may be used to direct expression of the polypeptide of the invention. The promoter may be selected for its efficiency in directing the expression of the polypeptide of the invention in the desired expression host.

A variety of promoters^{3,4} can be used that are capable of directing transcription in the host cells of the invention. Preferably the promoter sequence is derived from a highly
30 expressed gene as previously defined. Examples of preferred highly expressed genes from which promoters are preferably derived and/or which are comprised in preferred predetermined target loci for integration of expression constructs, include but are not

limited to genes encoding glycolytic enzymes such as triose-phosphate isomerases (TPI), glyceraldehyde-phosphate dehydrogenases (GAPDH), phosphoglycerate kinases (PGK), pyruvate kinases (PYK), alcohol dehydrogenases (ADH), as well as genes encoding amylases, glucoamylases, xylanases, cellobiohydrolases, β -galactosidases, alcohol (methanol) oxidases, elongation factors and ribosomal proteins. Specific examples of suitable highly expressed genes include e.g. the *LAC4* gene from *Kluyveromyces* sp., the methanol oxidase genes (*AOX* and *MOX*) from *Hansenula* and *Pichia*, respectively, the glucoamylase (*glaA*) genes from *A.niger* and *A.awamori*, the *A.oryzae* TAKA-amylase gene, the *A.nidulans* *gpdA* gene and the *T.reesei* cellobiohydrolase genes.

Examples of strong constitutive and/or inducible promoters which are preferred for use in fungal expression hosts are those which are obtainable from the fungal genes for xylanase (*xlnA*), phytase, ATP-synthetase, subunit 9 (*oliC*), triose phosphate isomerase (*tpi*), alcohol dehydrogenase (*AdhA*), α -amylase (*amy*), amyloglucosidase (AG - from the *glaA* gene), acetamidase (*amdS*) and glyceraldehyde-3-phosphate dehydrogenase (*gpd*) promoters.

Examples of strong yeast promoters are those obtainable from the genes for alcohol dehydrogenase, lactase, 3-phosphoglycerate kinase and triosephosphate isomerase.

Examples of strong bacterial promoters are the α -amylase and *SP02* promoters as well as promoters from extracellular protease genes.

20. Host cells and Expression

Preferably the polypeptide is produced as a secreted protein in which case the DNA sequence encoding a mature form of the polypeptide in the expression construct is operably linked to a DNA sequence encoding a signal sequence. Preferably the signal sequence is native (homologous) to the DNA sequence encoding the polypeptide. Alternatively the signal sequence is foreign (heterologous) to the DNA sequence encoding the polypeptide, in which case the signal sequence is preferably endogenous to the host cell in which the DNA sequence is expressed. Examples of suitable signal sequences for yeast host cells are the signal sequences derived from yeast α -factor genes. Similarly, a suitable signal sequence for filamentous fungal host cells is e.g. a signal sequence derived from a filamentous fungal (gluco)amylase gene, e.g. the *A.niger* *glaA* gene. This may be used in combination with the amyloglucosidase (AG) promoter itself, as well as in combination



with other promoters. Hybrid signal sequences may also be used with the context of the present invention.

Preferred heterologous secretion leader sequences are those originating from the fungal amyloglucosidase (AG) gene (*glaA* - both 18 and 24 amino acid versions e.g. from 5 *Aspergillus*), the α -factor gene (yeasts e.g. *Saccharomyces* and *Kluyveromyces*) or the α -amylase gene (*Bacillus*).

Downstream of the DNA sequence encoding the polypeptide, the expression construct preferably contains a 3' untranslated region containing one or more transcription termination sites, also referred to as a terminator. The origin of the terminator is less 10 critical. The terminator can e.g. be native to the DNA sequence encoding the polypeptide. However, preferably a yeast terminator is used in yeast host cells and a filamentous fungal terminator is used in filamentous fungal host cells. More preferably, the terminator is endo-genus to the host cell in which the DNA sequence encoding the polypeptide is expressed.

In a further aspect the invention provides a process for preparing polypeptides 15 according to the invention which comprises cultivating a host cell transformed or transfected with an expression vector as described above under conditions to provide for expression by the vector of a coding sequence encoding the polypeptides, and recovering the expressed polypeptides.

A further aspect of the invention thus provides host cells transformed or transfected 20 with or comprising a polynucleotide or vector of the invention. Preferably the polynucleotide is carried in a vector for the replication and expression of the polynucleotide. The cells will be chosen to be compatible with the said vector and may for example be prokaryotic (for example bacterial), fungal, yeast or plant cells.

Depending on the nature of the polynucleotide encoding the polypeptide of the 25 invention, and/or the desirability for further processing of the expressed protein, eukaryotic hosts such as yeasts or fungi may be preferred. In general, yeast cells are preferred over fungal cells because they are easier to manipulate. However, some proteins are either poorly secreted from yeasts, or in some cases are not processed properly (e.g. hyperglycosylation in yeast). In these instances, a fungal host organism should be selected.

30 A heterologous host may also be chosen wherein the polypeptide of the invention is produced in a form which is substantially free from other pectin-degrading enzymes. This may be achieved by choosing a host which does not normally produce such enzymes such

as *Kluyveromyces lactis*.

The invention encompasses processes for the production of the polypeptide of the invention by means of recombinant expression of a DNA sequence encoding the polypeptide. For this purpose the DNA sequence of the invention can be used for gene
5 amplification and/or exchange of expression signals, such as promoters, secretion signal sequences, in order to allow economic production of the polypeptide in a suitable homologous or heterologous host cell. A homologous host cell is herein defined as a host cell which is of the same species or which is a variant within the same species as the species from which the DNA sequence is derived.

10 Suitable host cells are preferably prokaryotic microorganisms such as bacteria, or more preferably eukaryotic organisms, for example fungi, such as yeasts or filamentous fungi, or plant cells.

Bacteria from the genus *Bacillus* are very suitable as heterologous hosts because of their capability to secrete proteins into the culture medium. Other bacteria suitable as hosts
15 are those from the genera *Streptomyces* and *Pseudomonas*. A preferred yeast host cell for the expression of the DNA sequence encoding the polypeptide is of the genera *Saccharomyces*, *Kluyveromyces*, *Hansenula*, *Pichia*, *Yarrowia*, and *Schizosaccharomyces*. More preferably a yeast host cell is selected from the group consisting of the species *Saccharomyces cerevisiae*, *Kluyveromyces lactis* (also known as *Kluyveromyces marxianus*
20 var. *lactis*), *Hansenula polymorpha*, *Pichia pastoris*, *Yarrowia lipolytica*, and *Schizosaccharomyces pombe*.

Most preferred for the expression of the DNA sequence encoding the polypeptide are, however, filamentous fungal host cells. Preferred filamentous fungal host cells are selected from the group consisting of the genera *Aspergillus*, *Trichoderma*, *Fusarium*, *Penicillium*,
25 *Acremonium*, *Neurospora*, *Thermoascus*, *Myceliophthora*, *Sporotrichum*, *Thielavia*, and *Talaromyces*. More preferably a filamentous fungal host cell is of the species *Aspergillus oryzae*, *Aspergillus sojae*, *Aspergillus nidulans*, species from the *Aspergillus niger* Group (as defined by Raper and Fennell, The Genus *Aspergillus*, The Williams & Wilkins Company, Baltimore, pp 293-344, 1965). These include but are not limited to *Aspergillus*
30 *niger*, *Aspergillus awamori*, *Aspergillus tubigenensis*, *Aspergillus aculeatus*, *Aspergillus foetidus*, *Aspergillus nidulans*, *Aspergillus japonicus*, *Aspergillus oryzae* and *Aspergillus ficuum*, and further consisting of the species *Trichoderma reesei*, *Fusarium graminearum*,

Penicillium chrysogenum, *Acremonium alabamense*, *Neurospora crassa*, *Myceliophthora thermophilum*, *Sporotrichum cellulophilum*, and *Thielavia terrestris*.

Examples of preferred expression hosts within the scope of the present invention are fungi such as *Aspergillus* species (described in EP-A-184,438 and EP-A-284,603) and
5 *Trichoderma* species; bacteria such as *Bacillus* species (described in EP-A-134,048 and EP-A-253,455), e.g. *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Pseudomonas* species; and yeasts such as *Kluyveromyces* species (described in EP-A-096,430 e.g. *Kluyveromyces lactic* and EP-A-301,670) and *Saccharomyces* species, e.g. *Saccharomyces cerevisiae*.

10 Culture of host cells and Recombinant production

According to the present invention, the production of the polypeptide of the invention can be effected by the culturing of microbial expression hosts, which have been transformed with one or more polynucleotides of the present invention, in a conventional nutrient fermentation medium.

15 The recombinant host cells according to the invention may be cultured using procedures known in the art. For each combination of a promoter and a host cell, culture condition are available which are conducive to the expression the DNA sequence encoding the polypeptide. After reaching the desired cell density or titre of the polypeptide the culture is stopped and the polypeptide is recovered using known procedures.

20 The fermentation medium can comprise a known culture medium containing a carbon source (e.g. glucose, maltose, molasses, etc.), a nitrogen source (e.g. ammonium sulphate, ammonium nitrate, ammonium chloride, etc.), an organic nitrogen source (e.g. yeast extract, malt extract, peptone, etc.) and inorganic nutrient sources (e.g. phosphate, magnesium, potassium, zinc, iron, etc.). Optionally, an inducer (e.g. apple MHR, pectin or
25 xylogalacturonan) may be included.

The selection of the appropriate medium may be based on the choice of expression host and/or based on the regulatory requirements of the expression construct. Such media are well-known to those skilled in the art. The medium may, if desired, contain additional components favouring the transformed expression hosts over other potentially
30 contaminating microorganisms.

The fermentation can be performed over a period of 0.5-20 days in a batch, continuous

or fed-batch process suitably at a temperature in the range of between 0 and 45°C and, for example, a pH between 2 and 10. Preferred fermentation conditions are a temperature in the range of between 20 and 37°C and/or a pH between 3 and 9. The appropriate conditions are usually selected based on the choice of the expression host and the protein to
5 be expressed.

After fermentation, the cells can be removed from the fermentation broth by means of centrifugation or filtration. After removal of the cells, the polypeptide of the invention may then be recovered and, if desired, purified and isolated by conventional means.

D. Methods of Processing Plant or Pectin-containing Materials

10 Plant and pectin-containing materials include plant pulp, parts of plants and plant extracts. In the context of this invention an extract from a plant material is any substance which can be derived from plant material by extraction (mechanical and/or chemical), processing or by other separation techniques. The extract may be juice, nectar, base, or concentrates made thereof. The plant material may comprise or be derived from
15 vegetables, e.g., carrots, celery, onions, legumes or leguminous plants (soy, soybean, peas) or fruit, e.g., pome or seed fruit (apples, pears, quince etc.), grapes, tomatoes, citrus (orange, lemon, lime, mandarin), melons, prunes, cherries, black currants, redcurrants, raspberries, strawberries, cranberries, pineapple and other tropical fruits, trees and parts thereof (e.g. pollen, from pine trees). According to this invention, apples and apple juice
20 are especially preferred.

The polypeptides of the invention can thus be used to treat plant material including plant pulp and plant extracts. For example, they may be used to treat apple pulp and/or raw juice during the production of apple juice. They may also be used to treat liquid or solid foodstuffs or edible foodstuff ingredients. Conveniently the polypeptide of the invention is
25 combined with suitable (solid or liquid) carriers or diluents including buffers to produce a composition or enzyme preparation.

The polypeptide is typically stably formulated either in liquid or dry form. Typically, the product is made as a composition which will optionally include, for example, a stabilising buffer and/or preservative. The compositions may also include other enzymes
30 capable of digesting plant material or pectin, for example other pectinases such as an endo-arabinanase, rhamnogalacturonases, and/or polygalacturonase. For certain

applications, immobilization of the enzyme on a solid matrix or incorporation on or into solid carrier particles may be preferred. The composition may also include a variety of other plant material-degrading enzymes, for example cellulases and other pectinases.

The polypeptides and compositions of the invention may therefore be used in a method of processing plant material to degrade or modify the pectin constituents of the cell walls of the plant material².

Typically, the polypeptides of the invention are used as a composition/ enzyme preparation as described above. The composition will generally be added to plant pulp obtainable by, for example mechanical processing such as crushing or milling plant material. Incubation of the composition with the plant will typically be carried out for at time of from 10 minutes to 5 hours, such as 30 minutes to 2 hours, preferably for about 1 hour. The processing temperature is preferably 10-55°C, e.g. from 15 to 25°C, optimally about 20°C and one can use 10-300g, preferably 30-70g, optimally about 50g of enzyme per ton of material to be treated. All the enzyme(s) or their compositions used may be added sequentially or at the same time to the plant pulp. Depending on the composition of the enzyme preparation the plant material may first be macerated (e.g. to a purée) or liquefied. Using the polypeptides of the invention processing parameters such as the yield of the extraction, viscosity of the extract and/or quality of the extract can be improved.

Alternatively, or in addition to the above, a polypeptide of the invention may be added to the raw juice obtained from pressing or liquefying the plant pulp. Treatment of the raw juice will be carried out in a similar manner to the plant pulp in respect of dosage, temperature and holding time. Again, other enzymes such as those discussed previously may be included. Typical incubation conditions are as described in the previous paragraph. Once the raw juice has been incubated with the polypeptides of the invention, the juice is then centrifuged or (ultra) filtered to produce the final product.

A composition containing a polypeptide of the invention may also be used during the preparation of fruit or vegetable purees.

The end product of these processes is typically heat-treated at 85°C for a time of from 1 minute to 1 hour, under conditions to partially or fully inactivate the polypeptides of the invention.

Due to the highly specific action on pectins the polypeptides of the invention may also be used to prepare pectins with modified characteristics, e.g. modified gelation capacities

for specific applications.

The polypeptides of the invention may also be added to animal feeds rich in pectin or xylogalacturonan, e.g. soy-containing food, to improve the breakdown of the plant cell wall leading to improved utilisation of the plant nutrients by the animal. The polypeptides of the invention may be added to the feed or silage if pre-soaking or wet diets are preferred. Advantageously, the polypeptides of the invention may continue to degrade xylogalacturonans in the feed *in vivo*. Fungal derived polypeptides of the invention in particular generally have lower pH optima and are capable of releasing important nutrients in such acidic environments as the stomach of an animal. The invention thus also contemplates (e.g. animal) feeds or foodstuffs comprising one or more polypeptides of the invention.

The polypeptides of the invention may also be used during the production of milk substitutes (or replacers) from soy bean. These milk substitutes can be consumed by both humans and animals. A typical problem during the preparation of these milk substitutes is the high viscosity of the soy bean slurry, resulting in the need for an undesirable dilution of the slurry to a concentration of dry solids of 10 to 15%. An enzyme preparation containing a polypeptide of the invention can be added to, or during the processing of, the slurry, enabling processing at a higher concentration (typically 40 to 50%) dry solids. The enzyme may also be used in the preparation of savoury product(s), e.g. from soy bean.

Assays for Pectin Degrading Enzymes

The novel assays and substrates described herein have allowed identification and confirmation of endo-xylogalacturonase activity. However, these assays can be used to detect other pectin degrading enzymes, whether or not they have endo-xylogalacturonase activity.

The substrate that can be used for this assay can comprise gum tragacanth which has been treated with a strong acid. A preferred acid is trifluoroacetic acid (TFA). The gum tragacanth may be optionally saponified and/or it may have been treated with an alkali, for example an alkali metal hydroxide, for example NaOH.

Another aspect of the invention relates to an assay for identifying or detecting a polypeptide which is able to degrade pectin. The activity may be an endo-xylogalacturonase or, may be pectin lyase, polygalacturonase, esterase, cellulase,

xyloglucanase, galactonase, arabinanase or rhamnogalacturonase. The assay may comprise:

- a. providing, as a substrate for a candidate compound (usually a polypeptide) the substrate described in the previous paragraph; and
- 5 b. contacting the substrate with the candidate compound, and detecting whether any reducing carbohydrates are produced.

The amount of these reducing carbohydrates can be measured. If necessary, they can then be compared to the amount of the carbohydrates produced in a control experiment, in the absence of candidate compound.

- 10 The measurement may involve a BCA assay. This may comprise measuring the amount of Cu(II) reduced to Cu(I) by the reducing carbohydrates present. This may be by contact with bicinchoninic acid (BCA), and determining the amount of BCA-Cu(I) complex formed.

- The invention will now be described with reference to the following Examples which
- 15 are intended to be illustrative only and not limiting. In the Figures which accompany the Examples:

- Figure 1 is a diagram of the hypothetical structure of the prevailing population of apple MHR (modified hairy region) having the highest molecular weight (subunit I is xylogalacturonan, subunit II is the backbone rich in arabinan side chains, subunit III is
- 20 rhamnogalacturonase oligomers. The distribution of acetyl groups is not presented but major parts are thought to be located within subunit III. Key: GalA = galacturonic acid; rham = rhamnose; gal=galactose; xyl = xylose; ara = arabinose);

Figure 2 is a map of the vector pCVlacK according to the invention (construction described in Example 1);

- 25 Figure 3 is a graph illustrating an HPAEC of xylogalacturonan after degradation by xylogalacturonase (a polypeptide of the invention);

Figure 4 is a graph illustrating an HPSEC of xylogalacturonan before and after degradation by a xylogalacturonase;

- 30 Figure 5 is a graph illustrating a Maldi-ToF mass spectrum of the products of complete degradation of xylogalacturonan by a xylogalacturonase;

Figures 6A-G are graphs of HPSEC elutions showing degradation of MHR-S by endo-arabinanase, rhamnogalacturonase and xylogalacturonase, separately and in

combination;

Figures 7 and 8 are graphs of a HPSEC and HPAEC, respectively, elution patterns showing degradation of soy pectin by xylogalacturonase; and

Figure 9 is a diagram showing the multiple alignment of the part of the PG, XghA and
5 RHG sequences (amino acids identical to the XghA sequence are replaced by a dot) and an introduction of gaps to obtain an optimal alignment are indicated (-). Conserved amino acids in all plant, fungal and prokaryotic PG's are shaded. Key: Atub = *A. tubigenis*; Anig = *A. niger*; Aac = *A. aculeatus*.

EXAMPLE 1

10 Construction of an *Aspergillus tubigenis* cDNA expression library

Example 1.1: Construction of an expression vector

Starting vector pGBHSA20 (CBS 997.96) contains the promoter and terminator sequence of the lactase gene (*lac4*) of *K. lactis*, a G418 selection marker and the *E. coli* plasmid pTZ18r for propagation in this host. The *K. lactis* KARSCEN cassette¹⁷ (a gift
15 from Dr. A.A. Winkler, Dept. of Cell Biology and Genetics, Leiden University, The Netherlands) was cloned in a unique *Sma*I site of this vector. The resulting vector was named pCVlacK (Figure 2). The unique *Hind*III and *Xho*I sites flanking the *lac4* promoter and terminator, respectively, can be used as cloning sites for cDNA synthesized from *Aspergillus tubigenis* poly(A) RNA.

20 Example 1.2: Isolation of poly(A) RNA and cDNA synthesis

Aspergillus tubigenis conidia were inoculated in triplicate at a density of 10^6 spores/ml in 300 ml of medium containing (per liter): 6 g NaNO₃, 0.5 g KCl, 1.5 g KH₂PO₄, 0.5 g MgSO₄ (pH6.5), 1 ml 1000x Timberlake spore elements (per ml, 50mg EDTA, 22mg FeSO₄.7H₂O, 5 mg MnCl₂.2H₂O, 22mg ZnSO₄.7H₂O, 1.6mg CuSO₄.5H₂O,
25 1.7mg CoCl₂.6H₂O, 1.5mg Na₂MoO₄.2H₂O, 11mg H₃BO₃, adjusted to pH 6.5) and 10ml 100x Timberlake vitamins (per ml, 0.2mg thiamine-HCl, 0.2mg riboflavin 0.2mg nicotinamide, 1mg pyridoxine-HCl, 0.02mg pantothenic acid, 0.4µm biotin, adjusted to pH 5 to 6), 1 g yeast extract, 5 g SoyoptimTM (defatted, toasted soy bean meal from Societé Industrielle Oleagineux, France). The cultures were incubated in a rotary shaker at 28°C,

150 rpm. The mycelium of one culture was harvested at 10 hours after inoculation, mycelium of the other two cultures at 16 and 24 hours after inoculation. From 1 g rinsed and squeezed mycelium total RNA was isolated by the RNazol method (Cinna/Biotechx). Poly(A) RNA was isolated using QiagenTM oligotex columns (Westburg). Equal amounts
5 of poly(A) RNA at time-points of 10, 16 and 24 hours were pooled. cDNA was synthesized using the ZAP-cDNA synthesis kit (StratageneTM) with the following modifications: the first-strand synthesis was done with Superscript II reverse transcriptase (GibcoBRL). To 7.5 µg poly(A) RNA, 2 µl linker-primer and RNase-free water was added to a final volume of 28.5 µl. This mixture was incubated for 10 minutes at 70°C and
10 chilled on ice. The following components were added: 10 µl 5x first strand buffer, 5 µl 0.1 M DTT, 3 µl first-strand methyl nucleotide mixture and 1 µl RNase block. This was incubated for 10 minutes at 25°C, followed by 2 minutes at 42°C. Subsequently, 2.5 µl SuperscriptTM II RT (200 U/µl) was added, mixed and incubated for 50 minutes at 42°C. A second modification of the protocol was ligation of a *Hind*III adaptor instead of the *Eco*RI
15 adaptor.

The cDNA pool was size separated using a Sephacryl S-500 column. The first fraction eluted from the column did not contain any cDNA but the second and third fraction contained the largest sized cDNA. Subsequent fractions were supposed to contain relatively higher amounts of non-full length cDNA and were of no use for construction of
20 the library. The cDNA of fractions 2 and 3 was ligated into the *Hind*III and *Xho*I sites of expression vector pCVlacK (see Figure 2) using the Clontech Ligation ExpressTM kit. Each ligation mixture was transformed in two batches to electrocompetent *E. coli* XL-Blue MRF'cells. The four transformation suspensions were plated onto 32 agar plates (LB + 50µg/ml ampicillin). After 16 hours of incubation at 37°C, 7366 transformants were
25 obtained. Bacteria were collected by pouring 2.5 ml LB medium onto a plate and then scraping off the cells; 0.5 ml of cell suspension was added to glycerol and stored at -80°C; the remaining 2 ml was used for DNA isolation (QiagenTM Spin miniprep kit). In case a low number of transformants per plate was found, the 2.5 ml was transferred to a second, third or fourth plate. This yielded 22 pools of about 325 individual transformants. Equal
30 amounts of DNA of each pool were combined for use in *K. lactis* transformation.

Example 1.3: Transformation of the expression library into *K. lactis*

An overnight culture of *K. lactis* strain CBS 2359 grown in YPD (10 g/l yeast extract, 20 g/l Bacto-peptone, 20 g/l glucose) at 30°C was diluted 3000-, 600-, 300- and 100-fold in 150 ml of fresh YPD and incubated for 6 hours at 30°C, 160 rpm in a rotary shaker. The culture with an optical density of 0.7-1.0 was used to prepare electrocompetent cells⁶.

- 5 Electrocompetent cells were transformed with 1 µg pooled DNA of the *E. coli* library. Electroporation was performed using a Biorad GenepulserTM with settings at 1.4 kV, 200 Ohm and 25 µF. Transformants were selected on double layer YPD plates (YPD with 20 g/l Bacto-agar): the bottom layer contained 50 µg/ml G418, the top layer was non-selective. 660 µL of transformation mix was plated onto 80 double layer plates.
- 10 Aliquots of 1.5 and 15 µL were pipetted onto the plates. About 10,000 transformants were obtained.

EXAMPLE 2

Substrate preparation

Example 2.1: Preparation of MHR-S from apples

- 15 Modified hairy regions (MHR) from apples were isolated as a filter retentate after treatment of apples with pectinase, and subsequently the MHR was saponified resulting in MHR-S^{*}.

Example 2.2: Synthesis of xylogalacturonan from gum tragacanth

- 5 g of gum tragacanth (Sigma, St. Louis, MO, USA) was suspended in 990 mL of ice-cold distilled water. To this solution 10 mL of an ice-cold 5 M NaOH solution was added. After 24 h, the saponified gum tragacanth (sGT) was dialysed extensively against distilled water at 4°C, and concentrated under reduced pressure to 1 L. For mild acid hydrolysis, 7.65 mL of trifluoric acid (TFA) was added to this sGT solution. Final concentration of TFA in the solution was 0.1 M. The sGT/TFA solution was heated to boiling point in a
- 25 microwave and subsequently incubated in a boiling water bath for 1 h. Finally the hydrolysate was dialyzed extensively against distilled water at 4°C and freeze-dried. This procedure yielded 2.61 g of material (further referred to as xylogalacturonan).

Example 2.3: Characterization of xylogalacturonan

To determine the sugar composition both from the original gum tragacanth as well as of the xylogalacturonan, samples were hydrolyzed with 1 M H₂SO₄ (100°C, 3 h)⁸ and neutral sugars were converted to their alditol acetates in order to quantify the individual sugars by Gas Chromatography (GC). The uronic acid content of the hydrolysate was determined colorimetrically using *m*-hydroxybiphenyl⁸. The sugar composition in mol% of the original gum tragacanth (GT) in comparison with the xylogalacturonan (XG) is shown in Table 1 below.

Table 1

Substrate	Sugar (mol%)						
	Rhamnose (Rha)	Fucose (Fuc)	Arabinose (Ara)	Xylose (Xyl)	Galactose (Gal)	Glucose (Glc)	Galacturonan (GalA)
GT	2	5	26	17	7	7	36
XG	3	0	1	25	9	6	56

The mild acid hydrolysis removed effectively arabinosyl and fucosyl residues from this polysaccharide, whereas the GalA:Xyl ratio was more or less unaltered.

The degree of acetyl and methyl esterification of gum tragacanth was estimated by High Pressure Liquid Chromatography (HPLC)⁷. The degree of methylation and acetylation of gum tragacanth is approximately 75% and 20%, respectively (calculated as mol methyl or acetyl groups per mol of GalA). Saponification of the gum removed all methyl and acetyl groups. Molecular weight distribution of the polymers was performed by High Pressure Size Exclusion Chromatography (HPSEC) on three Bio-Gel TSK columns (40XL, 30XL, and 20XL) in series⁸. Mild acid hydrolysis of saponified gum tragacanth was accompanied with a decrease in molecular weight, although the resulting material still had a high molecular weight. Based on HPSEC elution profiles, xylogalacturonan has an estimated molecular mass of approximately 1,100 kDa, using pullulan reference compounds.

Xylogalacturonan effectively proved to be resistant to enzymatic degradation by all tested endo-polygalacturonases and rhamnogalacturonases.

EXAMPLE 3

Screening the library with a BCA assay

Example 3.1: Growth of the transformants and enzyme preparation

From the about 10 000 *K. lactis* transformants produced in Example 1.3, 3,500 individual colonies were picked and transferred to separate wells of multi-well plates. The transformants in the multiwell plates were grown for 48 hours at 30°C in medium 1 (per 500 mL of H₂O (pH 6.0): mannitol, 10.00 g; NH₄H₂PO₄, 1.50 g; KH₂PO₄, 0.25 g; (NH₄)₂SO₄, 0.50 g; CaCl₂·2H₂O, 0.01 g; MgSO₄·7H₂O, 0.15 g; trace elements H₃BO₃, 375 µg; CuSO₄·5H₂O, 40 µg; KI, 75 µg; MnSO₄·4H₂O, 300 µg; Na₂MoO₄, 150 µg; ZnSO₄·7H₂O, 300 µg; FeCl₃·6H₂O, 200 µg) and vitamins Ca-pantothenate, 500 µg; thiamine, 500 µg; myo-inositol, 500 µg; pyridoxine, 500 µg; nicotinic acid, 500 µg; biotin, 5 µg) containing 80 ng/mL of the antibiotic G418 and the 35 plates were stored as 15% glycerol stocks.

These transformants were used to inoculate a new set of 35 multi-well plates containing 200 µL of the same medium with 80 ng/mL G418 with a replica plater. The *K. lactis* transformants were grown for two days at 30°C in a stove. The cells were precipitated by centrifugation at 3000 rpm in a Hermle™ zk380 centrifuge.

Example 3.2: Substrate degradation

Carefully, 25 µL of supernatant of each well was pipetted to a new multiwell plate, and 25 µL of a 0.2% solution of substrate (either MHR-S or xylogalacturonan or sGT/TFA from Example 2.2) or in 100 mM NaOAc buffer pH 5.0 was added. After incubation overnight in a stove at 30°C, the increase of reducing carbohydrates was measured with the BCA assay.

Example 3.3: The BCA assay

The BCA assay is based on the reduction of Cu(II) to Cu(I) by reducing carbohydrate mono- and oligomers. A complex is formed of bicinchoninic acid (BCA) and Cu(I). This complex produces an intense purple colour, which can be measured spectrophotometrically. This colour increases with an increasing reducing carbohydrate



concentration. The method used in this invention is a modification of a known method⁹ but was used for screening purposes.

The procedure consisted of mixing 10 μ L of reducing carbohydrate containing sample from Example 3.2 with 90 μ L of water and 100 μ L of BCA reagent together in a multi-well plate. BCA reagent was made freshly each day by mixing two solutions, A and B, 1:1 (v/v) together. Solution A consisted of 54.28 g Na_2CO_3 , 24.20 g NaHCO_3 and 1.942 g Na_2BCA per liter of distilled water. Solution B consisted of 1.248 g $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ and 1.262 g *L*-serine per liter of distilled water. The plate containing sample, reagent and water was incubated for one hour in a stove at 80°C with a lid on the plate. After cooling the plate for 15 minutes, the absorbance at 550 nm was measured using a multi-well plate reader (SLT lab instruments, Austria; model EAR 400). Testlines with galactose showed that the assay was linear in the range from 0 to 125 μ M galactose.

Transformants that produced in the BCA assay an absorbance 0.1 unit higher than the blank were checked for xylogalacturonan-degrading capabilities by growing them again and repeating the BCA assay using xylogalacturonan as a substrate. Three xylogalacturonase producing transformants were found.

EXAMPLE 4

Example 4.1: Characterization of xylogalacturonase encoding cDNA

All plasmid inserts of these three transformants were identical, as was found after analysis of the restriction patterns of these inserts. *K. lactis* transformant 27E8, exhibiting xylogalacturonase activity, was used to isolate the pCVlacK expression plasmid by a glass beads method¹⁰. After transformation and propagation of this plasmid in *E. coli*, the cDNA insert was excised from pCVlacK with a *Hind*III/*Xho*I digestion. This digestion released a 1.0 and 0.4 kb fragment, due to an internal *Hind*III site as appeared from the nucleotide sequence later on. The DNA sequence of the cDNA insert was determined on both strands using 5'- and 3'-specific primers to the *lac*-4 regulating sequences, and primers based on the cDNA sequence. The DNA sequence of the cDNA insert is presented in SEQ ID No. 1, together with the deduced amino acid sequence. Upstream of the ATG translation start codon, 20 nucleotides of 5'-untranslated sequence are present. Downstream the TAA stop codon 130 nucleotides non-translated sequence followed by the poly-A tail were found. The open reading frame of 1218 nucleotides (*xghA*) encodes a protein of 406 amino acids,

presented in SEQ ID No. 2, named XghA. The potential cleavage site of the signal sequence, predicted according to the (-3,-1) rule¹¹, is between position 18 and 19. The ORF, initiating with an ATG codon and terminating with a TAA codon is thus preceded by a 20 base pair 5'-noncoding region and followed by a 130 base pair 3'-noncoding region and a poly(A) tail. The sequence TCATCATGGC covering the ATG start codon closely resembles the contents of sequence for initiation of translation in higher eukaryotes¹⁴. The *xghA* cDNA encodes an apparent signal sequence of 18 amino acids at the amino terminus, with a signal peptidase cleavage site between Ala¹⁸ and Ala¹⁹. Two potential N-glycosylation sites have been found at Asn¹⁷⁸-Ser-Thr and Asn³⁰¹-Val-Thr.

Comparison of the amino acid sequence to protein databases showed homology to polygalacturonase sequences of prokaryotes, fungi, plants and to rhamnogalacturonases A and B of *Aspergillus*. A comparison of the XghA amino acid sequence has been made using sequences from the EMBL data library. XghA showed 31 to 39% similarity to the endo-PG's and 44% similarity to the exo-PG of *A. tubigensis*. Similarity of XghA to 2RHG-A's was 30% (*A. niger*) and 32% (*A. aculeatus*) whereas similarity to RGH-B of *A. niger* was only very limited.

Figure 9 shows the analysis of multiple alignments of Xgh to the PG's and to the RHG-A's. The multiple alignment shows four domains of conserved amino acids, which were first described for polygalacturonases of plant, fungal and bacterial origin¹⁵. When all the PG's that were recovered from a database search were aligned, only four small stretches of amino acids are conserved: NXD, DD, HG and RXK (shaded in Figure 9, where X represents a variable amino acid). Essential amino acids thought to be involved in the hydrolysis reaction are one of the three aspartic acid residues of domain I and II and the histidine of domain III. These domains are fully conserved in XghA. It is postulated that the fourth domain contains amino acids that are involved in substrate binding. The arginine residue of this domain is a glycine residue in XghA. The domains are less conserved in the RHG sequences, as only two of the three aspartic acid residues are conserved and the histidine is replaced by glycine.

Example 4.2: Southern blot analysis

The copy number of the *XghA* gene was determined by southern blot analysis of genomic DNA of *A. tubigensis* digested with several enzymes (results not shown).

Hybridization under stringent (65°C and 0.2 x SSC) and less stringent conditions (60°C and 1 x SSC) with a 1.0 kb *Hin* dIII fragment of *xghA* clearly showed single hybridizing fragments. This demonstrates that the *xghA* gene is present as a single copy in the *A. tubigenis* genome.

5 EXAMPLE 5

Expression of the enzyme

K. lactis transformants expressing the cDNA of endo-xylogalacturonase were transferred from multiwell plate glycerol stocks to reagent tubes: 10 µL glycerol stock was added to 1-2 mL of medium I (see Example 3.1) with 80 ng/mL of G418. These cultures
10 were grown at 30°C in a rotary incubator at 200 rpm for two days and used to inoculate Erlenmeyer flasks containing 20 mL of this same medium supplemented with antibiotic. For larger scale production of the enzyme, these cultures were used to inoculate 500 mL of the same medium supplemented with antibiotic in 1 L Erlenmeyer flasks. Cells were grown at 30°C in a rotary incubator at 200 rpm for two days. Cultures were centrifuged to
15 precipitate cells, the supernatant was used for the purification.

The crude enzyme preparation (350 mL) was preconcentrated on a Hitrap™ Q ion-exchange column (Pharmacia Biotech, Sweden) with a flow rate of 0.3 mL/min. Elution was performed on a FPLC system (Pharmacia Biotech, Sweden) with a salt gradient using a 20 mM piperazine (pH 5.0) starting buffer (buffer A) and a 0.5 M NaCl in
20 20 mM piperazine (pH 5.0) elution buffer (buffer B). The following gradient was used: to 10% B in 1 minute, to 35% B in 19 minutes, to 100% B in 2 minutes and 100% B for three more minutes. Activity was checked as described in Example 3 and active fractions were pooled. They were diluted three times with 20 mM piperazine buffer (pH 5.0) and applied on a MiniQ column (Pharmacia Biotech, Sweden). Elution was performed on a Smart
25 system (Pharmacia Biotech, Sweden) with a linear pH gradient from 20 mM piperazine (pH 5.0) starting buffer to 10 mM HCl a flow rate of 0.4 mL/min. Active fractions were pooled and investigated using SDS-PAGE. Upon silver staining of the gel one protein band with a molecular mass of approximately 60 kDa was found. The difference with the predicted MW of about 45 kDa, based on the DNA sequence (see Example 4) is thought to
30 be due to protein glycosylation.

EXAMPLE 6

Influences of pH and temperature on enzyme activity

Purified enzyme, obtained as described in Example 5, was used for the characterisation of the enzyme. Measurements at t=0 were used as blanks.

- 5 For the determination of the pH stability, the purified enzyme was preincubated without substrate for one hour at a pH range from 2.5 to 8 in McIlvaine buffers. Afterwards the enzyme was incubated with substrate for two hours and the increase in reducing sugars was determined as described in Example 3. The enzyme was stable over a pH range of 3 to 6.

- For the determination of the pH and temperature optima, the purified enzyme was
10 incubated with substrate for two hours at a pH range from 2.5 to 8 or a temperature range from 20 to 80°C. After this, the increase in reducing sugars was determined as described in Example 3. The enzyme has an optimum activity at a temperature of 60°C and at a pH of 3.0. The enzyme shows more than 50% of its activity in the pH range of 2.5 to 5.0. The activity at pH 2.5 was still 90% of the maximum value at pH 3.0. Values lower than pH
15 2.5 were not measured.

EXAMPLE 7

Mode of action of the xylogalacturonase

- Degradation of xylogalacturonan (modified gum tragacanth, Example 2.2) by the supernatant of the xylogalacturonase-producing *K. lactis* clone was monitored by high
20 performance anion exchange chromatography (HPAEC) and high performance size exclusion chromatography (HPSEC).

- HPAEC was performed using a Dionex carboxypack PA1 column of a size of 4 x 250 ml. Elution was performed with 0.1 M NaOH (solution A) and 1 M NaOAc in 0.1 NaOH (solution B). The following gradient was used: from 0 to 62% B in 50 minutes, to 100% B
25 in 5 minutes, followed by 100% B for 5 minutes. The enzyme did not produce xylose (expected at a retention time of 5 minutes) or galacturonic acid (expected at a retention time of 15 minutes), not even after 8 hrs incubation. Only oligomers were released, the smallest oligomer being found at a retention time of about 22 minutes: this was a xylose-galacturonic acid dimer. (In Figure 3, Bottom line (A): t=1h, middle line (B): t=4h,
30 top line (C): t=8h of incubation).

HPSEC was performed using three columns in series: Bio-Gel TSK 40 (300 x 7.5 mm, from Biorad), Bio-Gel TSK 30 XL (300 x 7.5 mm, from Biorad) and TSKGel G 2500 P

XL (300 x 7.8 mm, from TosoHaas). Figure 4 shows that the high molecular weight fraction of xylogalacturonan (left in the picture) was rapidly degraded (the top line (B) represents the polymer before degradation and the bottom line (A) represents the polymer after degradation).

- 5 When the degradation products were monitored by Maldi-ToF mass spectrometry the products found were identified and are shown in Table 2.

Table 2

Oligomers	Composition of Degradation Product	Peak Numbers (in Figure 4)	Molecular Weight (Da)
dimer	galAxyl	1	349.1
10 trimer	galA2xyl	2	525.1
tetramers	galA2xyl2, galA3xyl	3a, 3b	657.3, 701.3
pentamers	galA3xyl2, galA4xyl1	4a, 4b	833.4, 877.4
hexamer	galA4xyl2	5	1009.5
heptamers	galA4xyl3, galA5xyl2	6a, 6b	1141.6, 1185.5
15 octamer	galA6xyl2	7	1361.5

Two products were thus formed when MHR-S was incubated with XghA. These products appeared even after a short incubation time.

- These results show that xylogalacturonan is degraded by the xylogalacturonase in an endo-fashion. The profiles obtained were compared with those from a polygalacturonic acid digest, and it was clear that none of the MHR-S degradation products formed were polygalacturonic acid oligomers. This demonstrates that XghA produces galacturonic acid oligomers substituted with xylose.

Upon incubation of the supernatant of the xylogalacturonase producing *K.lactis* transformant with polygalacturonic acid no degradation of this substrate was observed.

25 EXAMPLE 8

Complete degradation of MHR-S by xylogalacturonase in combination with other enzymes

To study the degradation of MHR-S 200 μ L of a 0.3% MHR-S solution in 50 mM NaOAc buffer pH 5.0, was incubated with 5 μ L of the purified xylogalacturonase, 5 μ L of endo-arabinanase¹², 5 μ L of rhamnogalacturonase¹³, or with combinations of these enzymes, added sequentially or at the same time. MHR-S without enzyme was used as a control.

The degradation of MHR-S was monitored with HPSEC, as described in Example 7. The results are shown in Figures 6 to 6G where upper line (b) represents the control and the lower line (d) represents the incubations with enzyme. Incubations were with:

- 10 A: arabinanase;
- B: xylogalacturonase;
- C: rhamnogalacturonase;
- D: endo-arabinanase and xylogalacturonase sequentially;
- E: endo-arabinanase and xylogalacturonase combined;
- 15 F: endo-arabinanase and rhamnogalacturonase sequentially; and
- G: endo-arabinanase rhamnogalacturonase and xylogalacturonase combined.

Figure 6B shows that xylogalacturonase was able to degrade MHR-S: a small shift to lower molecular weight material can be observed. Also the enzymes endo-arabinanase (Figure 6A) and rhamnogalacturonase (Figure 6C) caused some shift in molecular weight. However, somewhat better results are obtained by combining two different enzymes in one incubation (Figures 6D - endo-arabinanase and xylogalacturonase sequentially; 20 6E - endo-arabinanase and xylogalacturonase combined and 6F - endo-arabinanase and endo-rhamnogalacturonase sequentially). The difference between Figures 6D and 6E is striking: combined addition of endo-arabinanase and xylogalacturonase was much more effective than with sequential addition. Almost complete degradation of the high 25 molecular weight material was possible when the three enzymes were added combined (Figure 6G).

EXAMPLE 9

Improvement of filtration rate by xylogalacturonase in combination with other enzymes

30 Experiments were done to see if the xylogalacturonase could prevent filterfouling during filtration. Apple MHR-S prepared as described in Example 2.1 was used as a

substrate. A solution of 0.5% in 50 mM acetate buffer pH 4.0 was incubated with a combination of three enzymes: endo-arabinanase, rhamnogalacturonase and xylogalacturonase (ea/rg/xgh), a combination of two enzymes: endo-arabinanase and rhamnogalacturonase (ea/rg), and with xylogalacturonase (xgh) separately for 17 hours at 30°C. The solutions were filtrated using an Amicon device equipped with a 30 kD filter at a pressure of 2 bars. The increase in weight of the filtrate was followed over time. The results are shown in Figure 5.

EXAMPLE 10

Degradation of a soy pectic fraction by xylogalacturonase

10 An Alkali soluble fraction of soybean meal, 1 MASS, rich in pectic substances was isolated and characterized¹⁶. A 0.25% solution of 1 MASS in 50mM sodium acetate buffer pH 5, including 0.01% NaN₃ was incubated with xylogalacturonase. The digest obtained after 24 hours of incubation at 30°C was analysed for the molecular weight distribution by HPSEC and the release of oligomeric degradation product by HPAEC. The analyses were
15 performed as described in Example 7.

Figure 7 shows the changes in the molecular weight distribution as measured by HPSEC: in the xylogalacturonase-treated material (curve b) the peak at approximately 20 min, representing the high molecular weight material, decreases to 70% of the value of the starting material (curve a).

20 In Figure 8 the results of the HPAEC analysis is shown. Comparing the enzyme-treated material (curve b) with the blank (curve a) it can be seen that xylogalacturonase causes the release of the characteristic xylosyl galacturonic acid dimer (marked with an X) and of other unidentified oligomers (peaks to the right side of X), comparable with the peaks appearing in Figure 6 of Example 7.

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CLAIMS

1. A polypeptide which possesses endo-xylogalacturonase activity.
2. A polypeptide having endo-xylogalacturonase activity which is obtainable from a fungus and possesses endo-xylogalacturonase activity.
- 5 3. A polypeptide according to claim 2 wherein said fungus is of the genus *Aspergillus*.
4. A polypeptide according to any preceding claim which comprises the sequence set out in SEQ ID No. 2, or a sequence substantially homologous thereto, or a fragment of either sequence.
- 10 5. A polypeptide according to claim 4 wherein the fragment has at least 5 amino acids or the homologous sequence is at least 60% identical to SEQ ID No. 2.
6. A polypeptide according to claim 5 which comprises amino acids 19 to 406 of the amino acid sequence set out in SEQ ID No. 2.
- 15 7. A polynucleotide encoding a polypeptide according to any one of the preceding claims.
8. A polynucleotide comprising:
 - (a) the polynucleotide sequence set out in SEQ ID No. 1, or the complement thereof;
 - (b) a polynucleotide sequence capable of hybridising to the nucleotide sequence set out in SEQ ID No. 1, or a fragment thereof;
 - 20 (c) a polynucleotide sequence capable of hybridising to the complement of the polynucleotide sequence set out in SEQ ID No. 1, or a fragment thereof; and/or
 - (d) a polynucleotide sequence which is degenerate as a result of the genetic code to any of the polynucleotides defined in (a), (b) or (c).
9. A polynucleotide according to claim 8 which:
 - 25 a. encodes a polypeptide having endo-xylogalacturonase activity, which polynucleotide is:
 - (1) the coding sequence of SEQ ID No. 1;
 - (2) a sequence which hybridises selectively to the complement of sequence defined in (1); or

(3) a sequence that is degenerate as a result of the genetic code with respect to a sequence defined in (1) or (2); or

b. is a sequence complementary to a polynucleotide defined in (a).

10. An isolated polynucleotide according to claim 7, 8 or 9 obtainable from a fungus.

5 11. A polynucleotide according to claim 10 wherein the fungus is of the genus *Aspergillus*.

12. A polynucleotide probe which comprises a fragment of at least 15 nucleotides of a polynucleotide as defined in any of claims 7 to 11.

13. A vector comprising a polynucleotide as defined in any one of claims 7 to 12.

10 14. An expression vector comprising a polynucleotide as defined in any one of claims 7 to 11 operably linked to one or more regulatory sequences capable of directing expression of the polynucleotide in a host cell.

15. A host cell transformed or transfected with, comprising or incorporating a vector according to any one of claims 13 to 14.

15 16. A host cell comprising or harbouring a polynucleotide according to any one of claims 7 to 11 wherein the polynucleotide is heterologous to the genome of the host cell.

17. A host cell according to claim 15 or claim 16 which is a yeast cell.

18. A method for producing a polypeptide according to any one of claims 1 to 6 which comprises incubating or culturing a host cell according to any one of claims 15 to 17
20 under conditions which allow the expression of the polypeptide, and optionally purifying the polypeptide.

19. A host cell comprising or expressing a polypeptide according to any one of claims 1 to 6 wherein the polypeptide is heterologous to the host cell.

20. A composition comprising a polypeptide according to any one of claims 1 to 6.

25 21. A composition according to claim 20 which further comprises a polypeptide having endo-arabinanase, rhamnogalacturonase or polygalacturonase activity.

22. A method of treating a plant material, the method comprising contacting the plant material with a polypeptide according to any one of claims 1 to 6 or a composition according to claim 20 or claim 21.

30 23. A method according to claim 22 wherein the treatment comprises degrading or modifying pectin in the plant material.

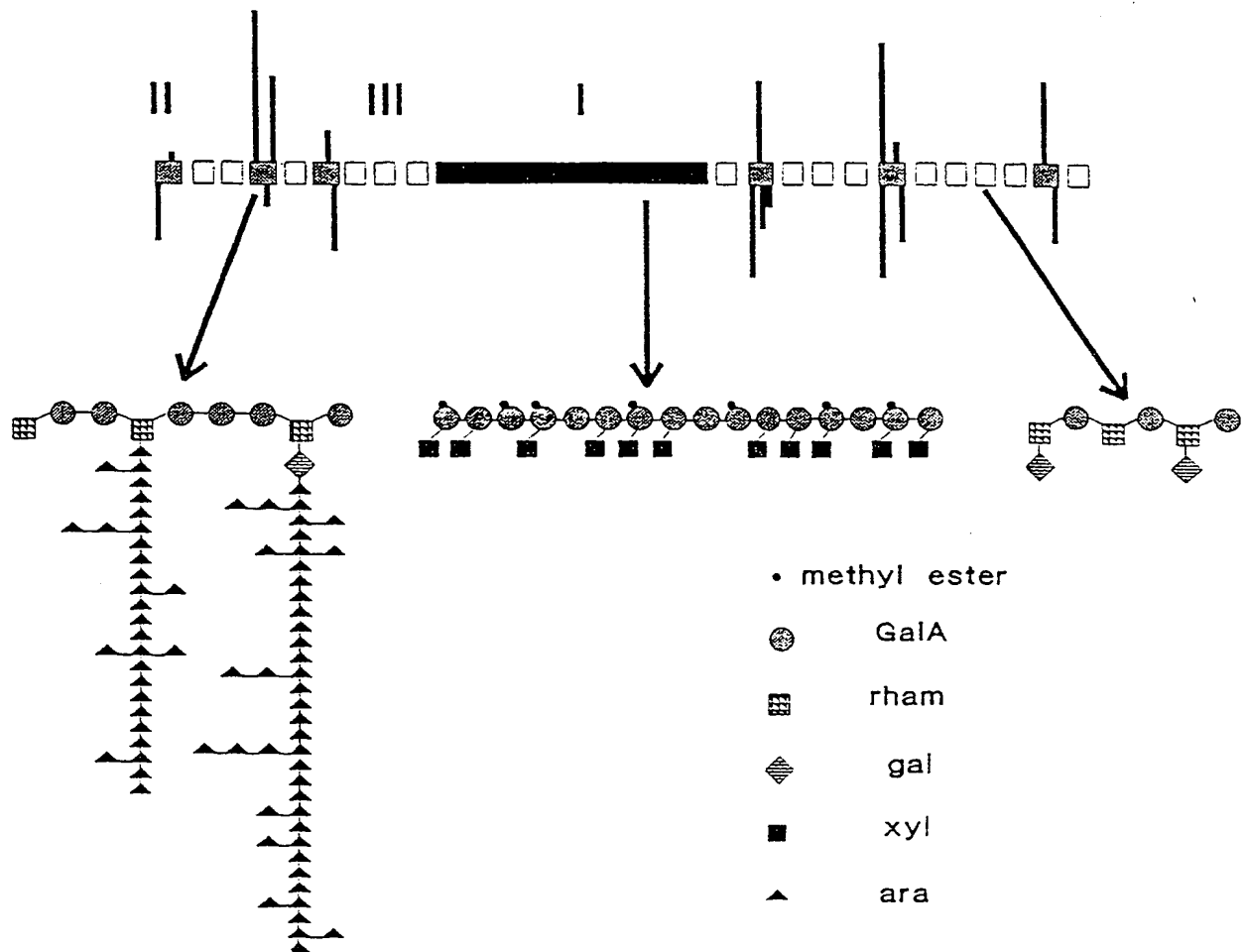
24. A method according to claim 22 for degrading or modifying plant cell walls.
25. A method according to claim 22 or 23 wherein the treatment comprises endo-type cleaving of xylogalacturonan subunits of a pectin component of the material.
26. A method according to any of claims 22 to 24 wherein the material comprises a
5 plant, plant pulp, plant extract or an edible foodstuff or ingredient therefor.
27. A method according to claim 26 wherein the material is fruit or vegetable pulp, juice or extract.
28. A processed plant material obtainable by contacting a plant material with a polypeptide according to any one of claims 1 to 6 or a composition according to claims 20
10 or claim 21, or which results from a method according to any of claim 22 to 26.
29. A processed plant material according to claim 27 which is a fruit or vegetable juice.
30. A method for reducing the viscosity of a plant material, the method comprising contacting the plant material with a polypeptide according to any one of claims 1 to 6 or a
15 composition according to claim 20 or claim 21 in an amount and under conditions effective to degrade pectin contained in the material.
31. Use of a polypeptide according to any one of claims 1 to 6 or a composition according to claim 20 or claim 21 in a method of treating plant material.
32. Use according to claim 31 wherein the treatment comprises endo-type cleaving
20 xylogalacturonan substituents of pectin in the plant material.
33. Use of a polypeptide according to any one of claims 1 to 6 or a composition according to claim 20 or claim 21 in a method of processing plant pulp, juice or extract which method comprises incubating the pulp, juice or extract with the polypeptide or composition to at least partially degrade pectin.
- 25 34. An (animal) feed or foodstuff comprising a polypeptide according to any one of the claims 1 to 6.
35. A composition comprising (optionally saponified) gum tragacanth (sGT) treated with a strong acid.
36. An assay for identifying or detecting a polypeptide having pectin degrading
30 activity, the assay comprising:
- a. providing, as a substrate for a candidate compound, (optionally saponified) gum tragacanth treated with a strong acid (sGT/TFA); and

b. contacting the sGT/TFA with the candidate compound and detecting whether any reducing carbohydrates are produced.

37. An assay according to claim 35 wherein the amount of reducing carbohydrates is measured and optionally compared to the amount of the carbohydrates produced in a control with the absence of the candidate compound.

38. An assay according to claim 35 or 36 which comprises measuring the amount of Cu(II) reduced to Cu(I) by the carbohydrates, optionally by contact with bicinchoninic acid (BCA) and determining the amount of BCA-Cu(I) complex formed.

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FIGURE 1

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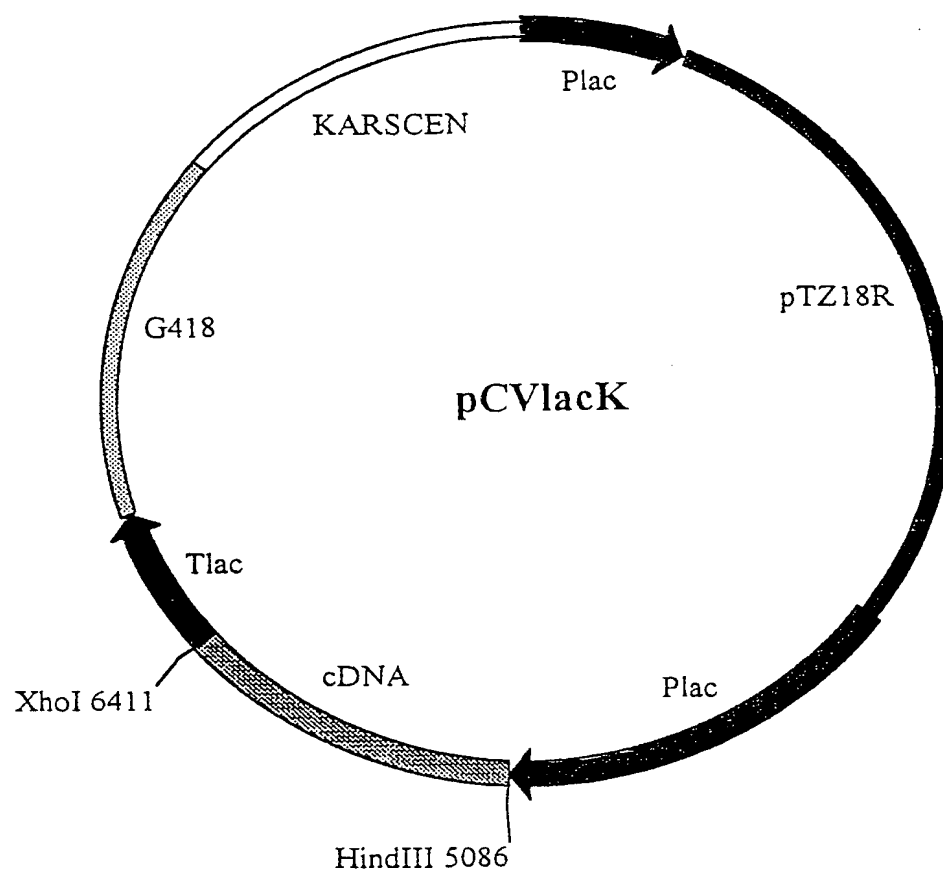
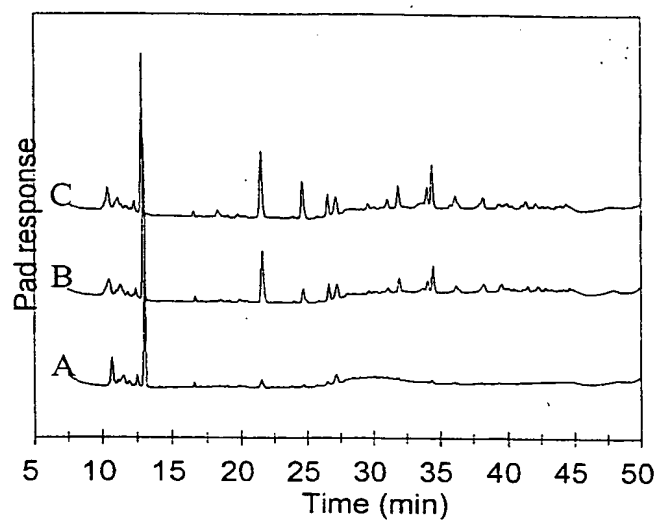
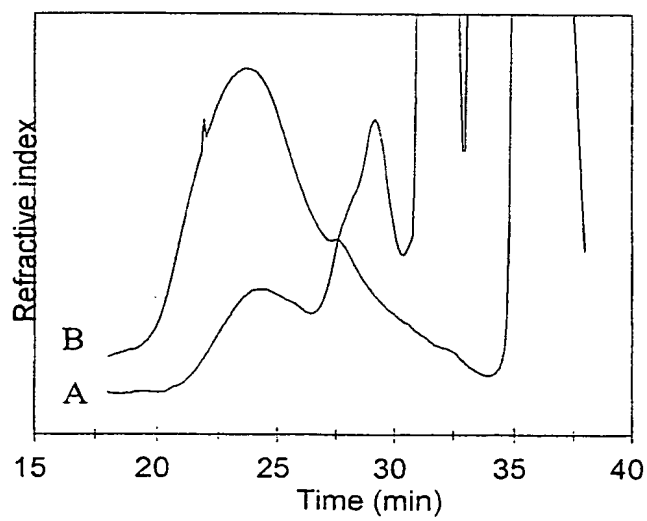


FIGURE 2

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FIGURE 3FIGURE 4

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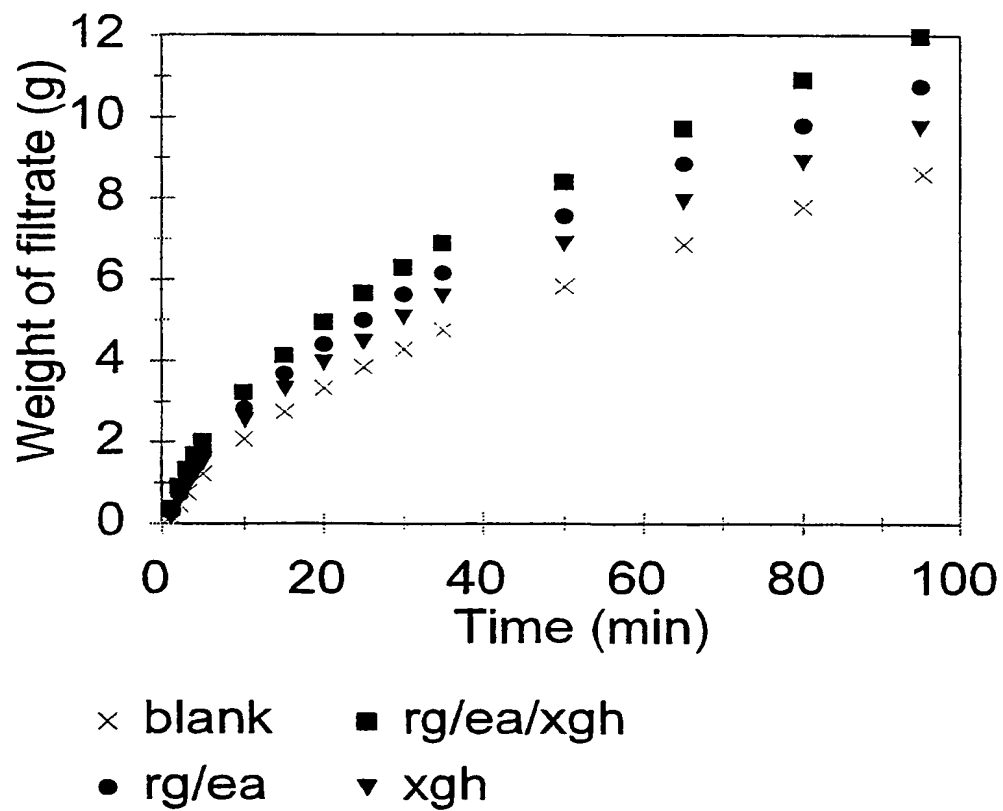
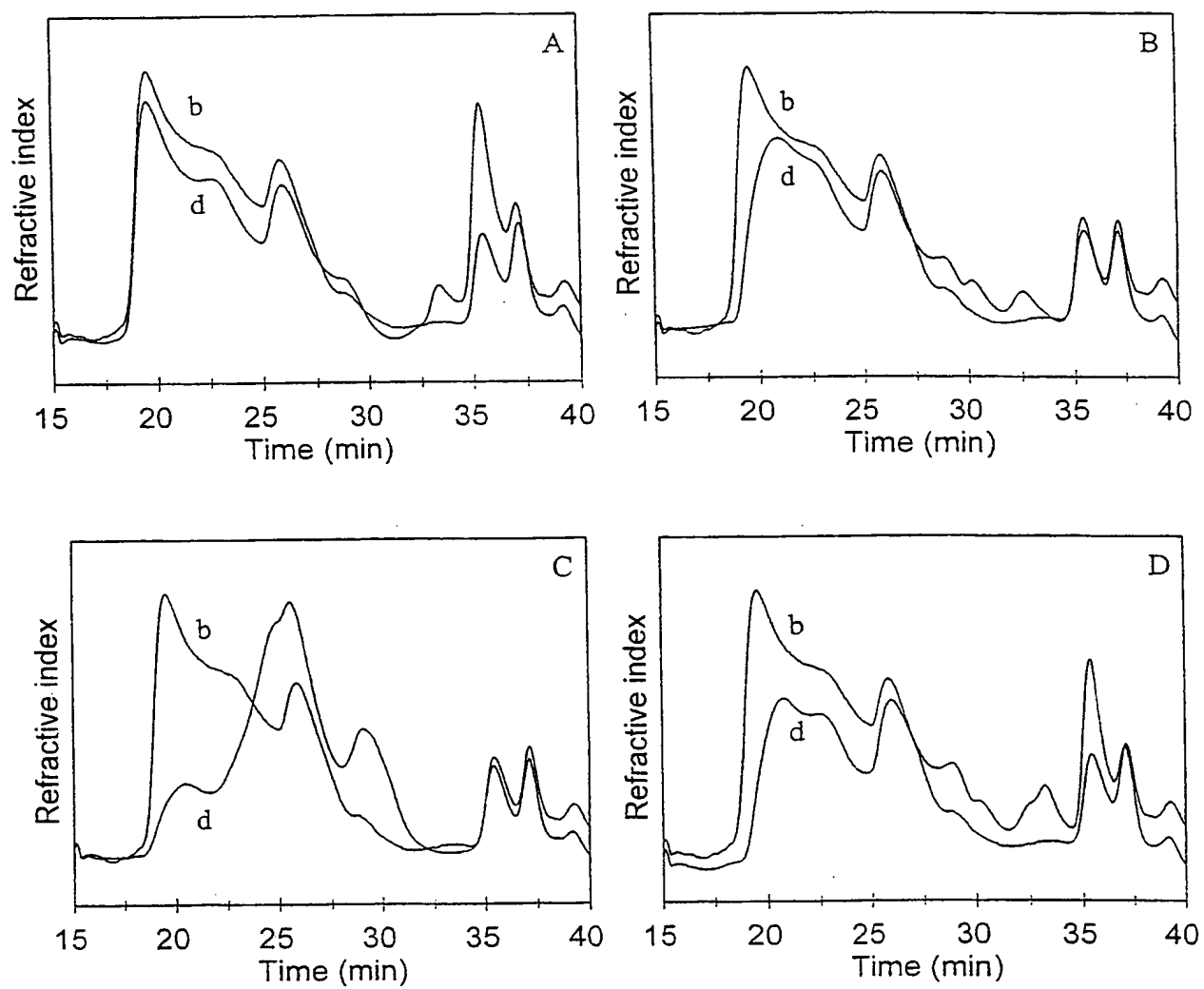
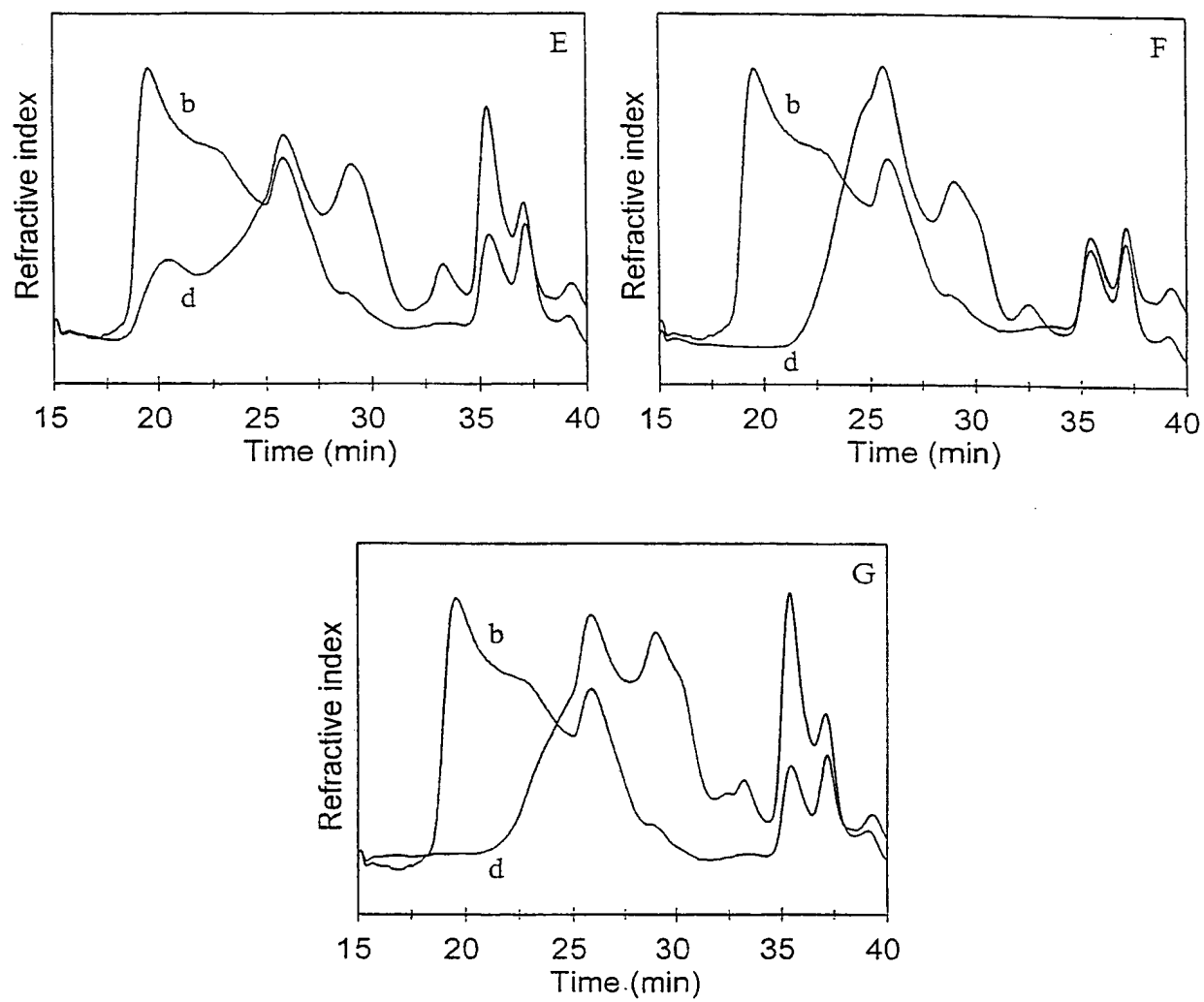


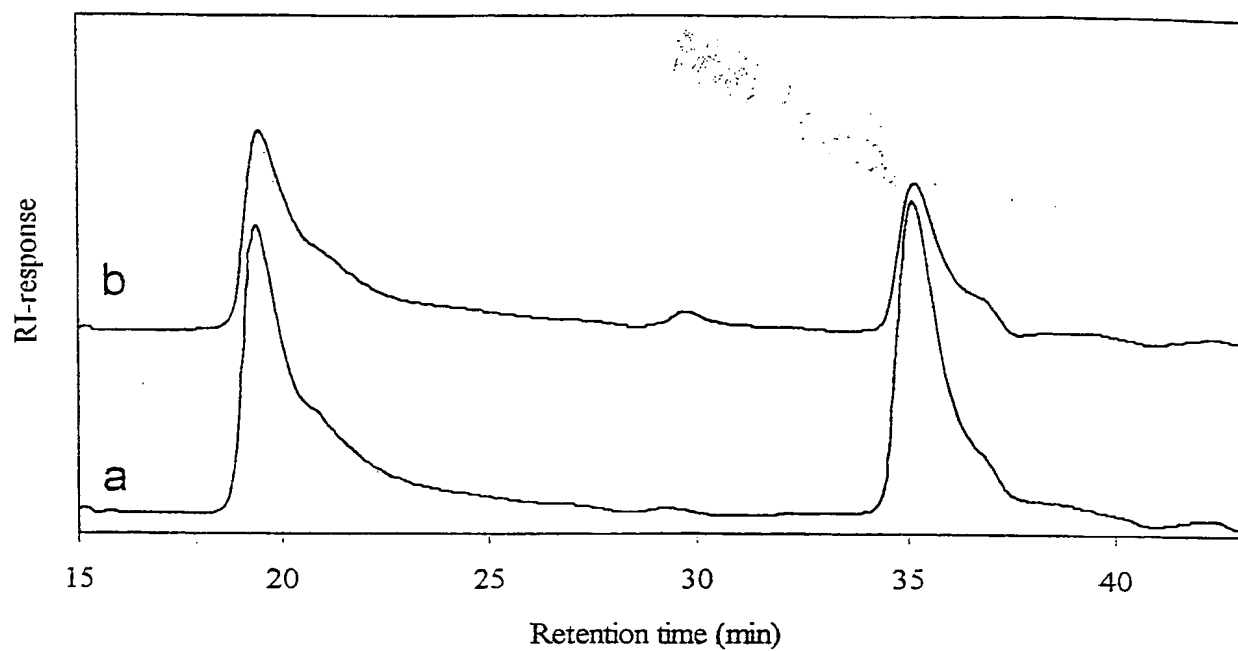
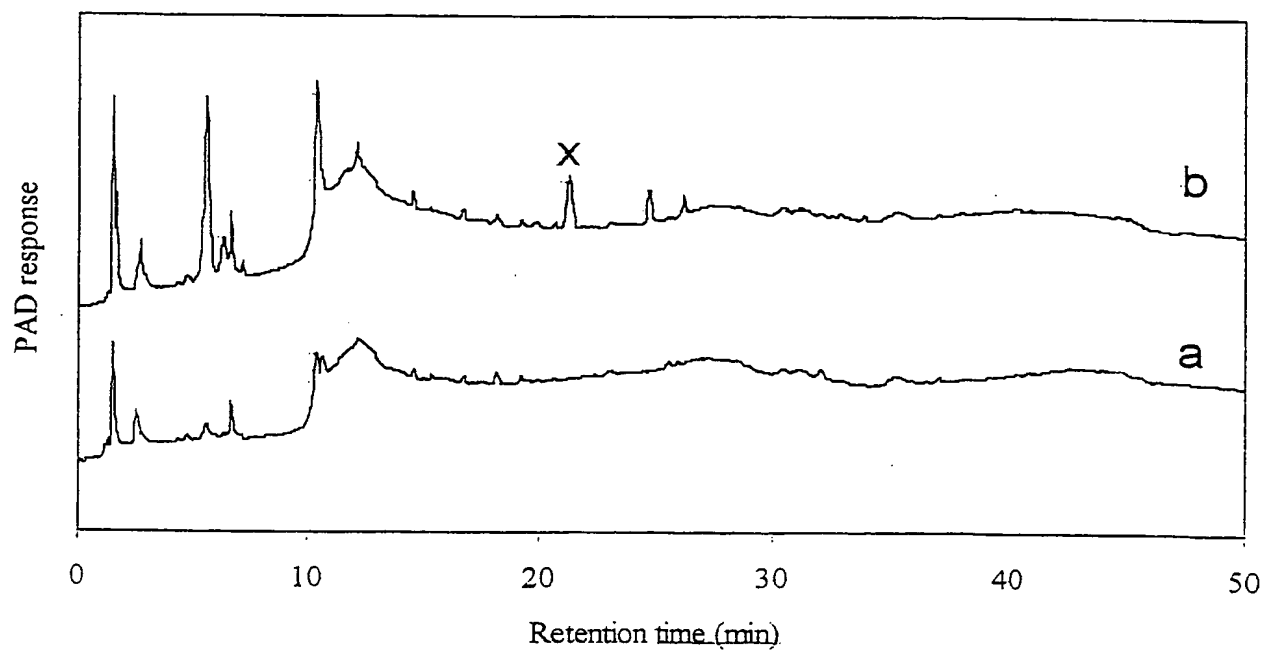
FIGURE 5

FIGURE 6A to 6D

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FIGURE 6E to 6G

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FIGURE 7FIGURE 8

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Atub-PgaII	173	TLGGH	A.	V.N.VG.N.	IKPW.H.Q.	II	L.IN-.GEN	IWFTSGT.I.	III	G.L.I..
Anig-PgaII	173	TQGGH	A.	V.N.VG.N.	IKPW.H.Q.		L.VN-.GEN	IWFTGGT.I.		G.L.I..
Anig-PgaI	179	..GGHSE..G.Y.	SGA..K.Q.		I.IN-.GES	ISFTGGT.S.		G.L.I..
Anig-PgaC	193	.DLAAI..	.GAEIY.Q.		...IN-.GEN	IYFSASV.S.		G.L.I..
Atub-PgaX	216	..EAK	..W	.TYR.NNIV.	QNSVIN.G		..S...NSTN	IL.QNLH.N.	
Atub-XghA	200	DNPPKNTDGF	DIGESTYVTI	TEVTVVNDEE			CVAFKPSSNY	VTVDTISCTG		SHGISVGS
Aac-RhgA	188	GGNEGGL	.I	.VWG.N-IWV	HD.E.T.K.E		..TV.SPA.N	IL.ES.Y.NW		.G.CAM..
Anig-RhgA	189	GGNSGGL	.I	.VWG.N-IWV	HD.E.T.K.E		..TV.GPA.N	IL.ES.Y.NW		.G.CAM..
Anig-RhgB	192	GGNHGGL	.I	.VWSNN-IWV	HD.E.T.K.E		.VTVKSP.KN	ILIES.Y.NW		.G.CGM..
Atub-PgaII	232	GR.N-NV..	.VTIEHS.VS	..EN.VR	IV	VSGATGSVSE	ITYSNIVMSG	IS.YGVVIQ		
Anig-PgaII	232	DR.N-NV..	.VTIEHS.VS	..EN.VR		ISGATGSVSE	ITYSNIVMSG	IS.YGVVIQ		
Anig-PgaI	238	GRD.--NT..	.VTISDS.VS	.SANGVR		IYKETGDSVSE	ITYSNIQLSG	IT.YGIVIE		
Anig-PgaC	252	GRD.--NT..	.VTFYDVNVL	K.QQ.IR		IYGDTGSVSE	VTYHEIAFSD	AT.YGIVIE		
Atub-PgaX	276	QYK.EV.I.E	.V..YNISMF	.ASDM.R..		W.GTPSALSA	DLQGGGSGS	VKN--ITYD		
Atub-XghA	260	KSSD--DSVK	NIYVTGATMI	NSTKAAGIKI		YPSGGDHGTS	TVSNVTFNDF	TVDNSDYAF		
Aac-RhgA	247	--A.--TD.T	D.VYRNVTW	S.NQMYM	S	-----NG.SGLLEN.	IGHGNA.SI		
Anig-RhgA	248	--A.--TDIT	D.LYRNVTW	S.NQMYM	S	-----NG.SG	..N.TLLEN.	IGRGNR.SI		
Anig-RhgB	251	--S.--TN.S	D.TYRNIYTW	S.NNMML	S	-----NG.SG	F.E..LLEN.	IGHGNA.SI		

FIGURE 9

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- 1 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- 5 (A) NAME: Gist-brocades B.V.
 (B) STREET: Wateringseweg 1
 (C) CITY: Delft
 (E) COUNTRY: the Netherlands
 (F) POSTAL CODE (ZIP): 2611 XT

(ii) TITLE OF INVENTION: Novel Endo-xylogalacturonase

10 (iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER READABLE FORM:

- 15 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: N/A

(2) INFORMATION FOR SEQ ID NO:1:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1602 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus tubigensis*

30 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 98..1318 CTCGAG is XhoI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	GCTTGTGTTT CTTAGGAGAA TTATTATTCT TTTGTTATGT TGCGCTTGTA GTTGAAAAG	60
35	GTGAAGAGAC AAAGCTTGAA TTCCGAAATC GCTCATC ATG GCG CTA TAT CGT AAC	115
	Met Ala Leu Tyr Arg Asn	
	1 5	
	CTC TAC CTT CTG GCC AGC CTT GGG CTA AGC AGT GCT GCT CCC TCC AAG	163
40	Leu Tyr Leu Leu Ala Ser Leu Gly Leu Ser Ser Ala Ala Pro Ser Lys	
	10 15 20	

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	GTC	CAG	CGA	GCC	CCG	GAT	TCT	TCC	ATT	CAT	GCT	CGC	GCT	GTC	TGT	ACC	211
	Val	Gln	Arg	Ala	Pro	Asp	Ser	Ser	Ile	His	Ala	Arg	Ala	Val	Cys	Thr	
			25					30					35				
5	CCG	ACC	GCA	GGA	GGC	GAT	TCG	TCC	ACC	GAC	GAT	GTC	CCC	GCC	ATC	ACC	259
	Pro	Thr	Ala	Gly	Gly	Asp	Ser	Ser	Thr	Asp	Asp	Val	Pro	Ala	Ile	Thr	
		40					45					50					
	GAG	GCC	CTC	AGC	TCG	TGC	GGA	AAT	GGT	GGC	ACC	ATC	GTC	TTC	CCC	GAG	307
	Glu	Ala	Leu	Ser	Ser	Cys	Gly	Asn	Gly	Gly	Thr	Ile	Val	Phe	Pro	Glu	
	55					60					65					70	
10	GGC	AGC	ACC	TAC	TAC	CTC	AAC	AGT	GTG	CTG	GAC	TTG	GGC	AGC	TGC	AGT	355
	Gly	Ser	Thr	Tyr	Tyr	Leu	Asn	Ser	Val	Leu	Asp	Leu	Gly	Ser	Cys	Ser	
					75					80					85		
15	GAT	TGC	GAC	ATC	CAG	GTG	GAA	GGT	CTT	CTG	AAG	TTC	GCC	AGC	GAT	ACC	403
	Asp	Cys	Asp	Ile	Gln	Val	Glu	Gly	Leu	Leu	Lys	Phe	Ala	Ser	Asp	Thr	
				90					95					100			
	GAT	TAC	TGG	AGC	GGT	CGC	ACT	GCC	ATG	ATC	AGT	GTT	TCC	AAT	GTA	GAT	451
	Asp	Tyr	Trp	Ser	Gly	Arg	Thr	Ala	Met	Ile	Ser	Val	Ser	Asn	Val	Asp	
			105					110					115				
20	GGT	TTG	AAG	CTG	CGC	TCA	TTG	ACT	GGA	TCT	GGT	GTC	ATT	GAT	GGC	AAT	499
	Gly	Leu	Lys	Leu	Arg	Ser	Leu	Thr	Gly	Ser	Gly	Val	Ile	Asp	Gly	Asn	
		120					125					130					
	GGC	CAG	GAT	GCG	TGG	GAT	CTC	TTT	GCT	TCG	GAC	AGT	AGT	TAC	TCA	CGC	547
	Gly	Gln	Asp	Ala	Trp	Asp	Leu	Phe	Ala	Ser	Asp	Ser	Ser	Tyr	Ser	Arg	
	135					140					145					150	
25	CCG	ACG	CTC	TTG	TAC	ATC	ACT	GGC	GGC	AGC	AAC	CTA	GAA	ATC	TCC	GGG	595
	Pro	Thr	Leu	Leu	Tyr	Ile	Thr	Gly	Gly	Ser	Asn	Leu	Glu	Ile	Ser	Gly	
					155					160					165		
30	CTG	CGT	CAA	AAG	AAT	CCA	CCT	AAC	GTG	TTC	AAC	TCG	GTC	AAG	GGT	GGC	643
	Leu	Arg	Gln	Lys	Asn	Pro	Pro	Asn	Val	Phe	Asn	Ser	Val	Lys	Gly	Gly	
				170					175					180			
	GCC	ACT	AAT	GTC	GTC	TTC	TCC	AAC	CTG	AAG	ATG	GAT	GCC	AAC	TCC	AAG	691
	Ala	Thr	Asn	Val	Val	Phe	Ser	Asn	Leu	Lys	Met	Asp	Ala	Asn	Ser	Lys	
			185					190					195				
35	TCG	GAC	AAT	CCG	CCC	AAG	AAC	ACT	GAT	GGG	TTC	GAC	ATT	GGC	GAG	AGT	739
	Ser	Asp	Asn	Pro	Pro	Lys	Asn	Thr	Asp	Gly	Phe	Asp	Ile	Gly	Glu	Ser	
		200					205					210					
	ACC	TAT	GTG	ACC	ATC	ACC	GAG	GTC	ACC	GTA	GTC	AAC	GAT	GAC	GAC	TGT	787
	Thr	Tyr	Val	Thr	Ile	Thr	Glu	Val	Thr	Val	Val	Asn	Asp	Asp	Asp	Cys	
	215					220					225					230	
40	GTC	GCC	TTC	AAG	CCC	AGT	TCC	AAC	TAC	GTG	ACA	GTG	GAC	ACG	ATC	AGC	835
	Val	Ala	Phe	Lys	Pro	Ser	Ser	Asn	Tyr	Val	Thr	Val	Asp	Thr	Ile	Ser	
					235					240					245		
	TGC	ACC	GGC	TCC	CAT	GGA	ATT	TCC	GTG	GGA	TCA	TTA	GGA	AAG	TCG	AGC	883
	Cys	Thr	Gly	Ser	His	Gly	Ile	Ser	Val	Gly	Ser	Leu	Gly	Lys	Ser	Ser	

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	250	255	260	
	GAC GAC TCG GTC AAG AAC ATT TAT GTC ACG GGC GCA ACT ATG ATC AAC			931
	Asp Asp Ser Val Lys Asn Ile Tyr Val Thr Gly Ala Thr Met Ile Asn			
	265	270	275	
5	TCC ACC AAA GCC GCC GGG ATC AAG ACT TAT CCG AGT GGA GGC GAC CAC			979
	Ser Thr Lys Ala Ala Gly Ile Lys Thr Tyr Pro Ser Gly Gly Asp His			
	280	285	290	
	GGT ACC TCC ACG GTC AGC AAT GTG ACC TTC AAC GAT TTC ACT GTG GAC			1027
	Gly Thr Ser Thr Val Ser Asn Val Thr Phe Asn Asp Phe Thr Val Asp			
10	295	300	305	310
	AAC TCC GAC TAT GCC TTC CAG ATC CAG AGC TGC TAT GGC GAG GAC GAT			1075
	Asn Ser Asp Tyr Ala Phe Gln Ile Gln Ser Cys Tyr Gly Glu Asp Asp			
	315	320	325	
	GAC TAT TGC GAG GAA AAC CCG GGC AAC GCC AAA CTG ACT GAT ATA GTC			1123
15	Asp Tyr Cys Glu Glu Asn Pro Gly Asn Ala Lys Leu Thr Asp Ile Val			
	330	335	340	
	GTG TCA AGC TTC AGT GGG ACA ACC AGT GAC AAG TAC GAT CCG GTC GTG			1171
	Val Ser Ser Phe Ser Gly Thr Thr Ser Asp Lys Tyr Asp Pro Val Val			
	345	350	355	
20	GCC AAC CTC GAC TGC GGT GCG GAT GGA ACT TGT GGC ATC TCC ATC AGT			1219
	Ala Asn Leu Asp Cys Gly Ala Asp Gly Thr Cys Gly Ile Ser Ile Ser			
	360	365	370	
	GGG TTC GAT GTC AAG GCG CCA TCG GGC AAG TCT GAA GTG TTG TGC GCC			1267
	Gly Phe Asp Val Lys Ala Pro Ser Gly Lys Ser Glu Val Leu Cys Ala			
25	375	380	385	390
	AAC ACC CCG TCT GAT TTG GGC GTC ACT TGC ACT TCG GGG GCT TCG GGC			1315
	Asn Thr Pro Ser Asp Leu Gly Val Thr Cys Thr Ser Gly Ala Ser Gly			
	395	400	405	
	TAAATAGCTT TGGCCGGGTT GCTTTCTGAA TCCACTGAGT GGAGGTCTTC TTCGGGTTTG			1375
30	ATATTTTGTA TGGTCGTGTG TATAGCAGAA TGTGACAATA GAATTAGTGA AATTGCCATT			1435
	CTTTTCGAAA GACAAAAAAA AAAAAAAAAA AAAAAAAAAA ACTCGAGAAT TTATACTTAG			1495
	ATAAGTATGT ACTTACAGGT ATATTTCTAT GAGATACTGA TGTATACATG CATGATAATA			1555
	TTTAAACGGT TATTAGTGCC GATTGTCTTG TGCGATAATG ACGTTCC			1602

(2) INFORMATION FOR SEQ ID NO:2:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 406 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	Ala	Leu	Tyr	Arg	Asn	Leu	Tyr	Leu	Leu	Ala	Ser	Leu	Gly	Leu	Ser	
	1				5					10					15		
5	Ser	Ala	Ala	Pro	Ser	Lys	Val	Gln	Arg	Ala	Pro	Asp	Ser	Ser	Ile	His	
				20					25					30			
	Ala	Arg	Ala	Val	Cys	Thr	Pro	Thr	Ala	Gly	Gly	Asp	Ser	Ser	Thr	Asp	
				35				40					45				
	Asp	Val	Pro	Ala	Ile	Thr	Glu	Ala	Leu	Ser	Ser	Cys	Gly	Asn	Gly	Gly	
		50					55					60					
10	Thr	Ile	Val	Phe	Pro	Glu	Gly	Ser	Thr	Tyr	Tyr	Leu	Asn	Ser	Val	Leu	
	65					70				75						80	
	Asp	Leu	Gly	Ser	Cys	Ser	Asp	Cys	Asp	Ile	Gln	Val	Glu	Gly	Leu	Leu	
					85					90					95		
15	Lys	Phe	Ala	Ser	Asp	Thr	Asp	Tyr	Trp	Ser	Gly	Arg	Thr	Ala	Met	Ile	
				100					105					110			
	Ser	Val	Ser	Asn	Val	Asp	Gly	Leu	Lys	Leu	Arg	Ser	Leu	Thr	Gly	Ser	
				115				120					125				
	Gly	Val	Ile	Asp	Gly	Asn	Gly	Gln	Asp	Ala	Trp	Asp	Leu	Phe	Ala	Ser	
		130					135				140						
20	Asp	Ser	Ser	Tyr	Ser	Arg	Pro	Thr	Leu	Leu	Tyr	Ile	Thr	Gly	Gly	Ser	
	145					150					155					160	
	Asn	Leu	Glu	Ile	Ser	Gly	Leu	Arg	Gln	Lys	Asn	Pro	Pro	Asn	Val	Phe	
					165					170					175		
25	Asn	Ser	Val	Lys	Gly	Gly	Ala	Thr	Asn	Val	Val	Phe	Ser	Asn	Leu	Lys	
				180					185					190			
	Met	Asp	Ala	Asn	Ser	Lys	Ser	Asp	Asn	Pro	Pro	Lys	Asn	Thr	Asp	Gly	
			195					200					205				
	Phe	Asp	Ile	Gly	Glu	Ser	Thr	Tyr	Val	Thr	Ile	Thr	Glu	Val	Thr	Val	
		210					215					220					
30	Val	Asn	Asp	Asp	Asp	Cys	Val	Ala	Phe	Lys	Pro	Ser	Ser	Asn	Tyr	Val	
	225					230					235					240	
	Thr	Val	Asp	Thr	Ile	Ser	Cys	Thr	Gly	Ser	His	Gly	Ile	Ser	Val	Gly	
					245					250					255		
35	Ser	Leu	Gly	Lys	Ser	Ser	Asp	Asp	Ser	Val	Lys	Asn	Ile	Tyr	Val	Thr	
				260					265					270			
	Gly	Ala	Thr	Met	Ile	Asn	Ser	Thr	Lys	Ala	Ala	Gly	Ile	Lys	Thr	Tyr	
			275					280					285				
	Pro	Ser	Gly	Gly	Asp	His	Gly	Thr	Ser	Thr	Val	Ser	Asn	Val	Thr	Phe	
		290					295					300					

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Asn Asp Phe Thr Val Asp Asn Ser Asp Tyr Ala Phe Gln Ile Gln Ser
 305 310 315 320
 Cys Tyr Gly Glu Asp Asp Asp Tyr Cys Glu Glu Asn Pro Gly Asn Ala
 325 330 335
 5 Lys Leu Thr Asp Ile Val Val Ser Ser Phe Ser Gly Thr Thr Ser Asp
 340 345 350
 Lys Tyr Asp Pro Val Val Ala Asn Leu Asp Cys Gly Ala Asp Gly Thr
 355 360 365
 10 Cys Gly Ile Ser Ile Ser Gly Phe Asp Val Lys Ala Pro Ser Gly Lys
 370 375 380
 Ser Glu Val Leu Cys Ala Asn Thr Pro Ser Asp Leu Gly Val Thr Cys
 385 390 395 400
 Thr Ser Gly Ala Ser Gly
 405

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INTERNATIONAL SEARCH REPORT

International Application No
PC1/EP 99/00860

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/55 C12N9/24 C12P21/00 C12Q1/34 A23L1/0524
A23L1/06

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N A23L

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	CHEN W P ET AL.: "Purification and some properties of beta-1,3-xylanases from <i>Aspergillus terreus</i> A-07. Endo-1,3-beta-D-xylanase isolation and characterization" AGRICULTURAL AND BIOLOGICAL CHEMISTRY., vol. 50, no. 5, 1986, pages 1183-1194, XP002111869 TOKYO., JP ISSN: 0002-1369 page 1183 -page 1187 --- -/--	1-3

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *Z* document member of the same patent family

Date of the actual completion of the international search

18 August 1999

Date of mailing of the international search report

24 NOV. 1999

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentaan 2
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Fax: (+31-70) 340-3016

Authorized officer

De Kok, A

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 99/00860

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	RENARD C.M.G.C. ET AL.: "The xylose-rich pectins from pae hulls" INTERNATIONAL JOURNAL OF BIOLOGICAL MACROMOLECULES, vol. 21, no. 1-2, August 1997 (1997-08), pages 155-162, XP002112536 AMSTERDAM NL abstract page 161, column 2 -page 162 ---	1
A	SCHOLS H A ET AL: "A xylogalacturonan subunit present in the modified hairy regions of apple pectin" CARBOHYDRATE RESEARCH, vol. 279, 27 December 1995 (1995-12-27), page 265-279 XP004018802 amsterdam nl ISSN: 0008-6215 abstract page 277, last paragraph ---	1
A	WO 94 14966 A (GIST BROCADES) 7 July 1994 (1994-07-07) page 1 -page 8 ---	1-3, 20-34
A	EP 0 421 919 A (CIBA GEIGY AG) 10 April 1991 (1991-04-10) page 1 -page 18 ---	1,2,7, 12-17, 19,22-34
A	WO 95 34223 A (NOVONORDISK AS) 21 December 1995 (1995-12-21) page 1, line 1 -page 6, line 16 -----	1

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INTERNATIONAL SEARCH REPORT

Int. application No.
PCT/EP 99/00860

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-34

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

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This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-34

An endo-xylogalacturonase, nucleic acids encoding it, vectors and hosts containing said nucleic acids and their use.

2. Claims: 35-38

An assay for identifying or detecting a polypeptide having pectin degrading activity and composition for use in this method.

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INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 99/00860

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9414966 A	07-07-1994	BR 9305957 A	21-10-1997
		EP 0628081 A	14-12-1994
		FI 943866 A	23-08-1994
		JP 7503861 T	27-04-1995
		PL 304896 A	09-01-1995
		US 5624834 A	29-04-1997
		US 5830737 A	03-11-1998
EP 0421919 A	10-04-1991	AU 640405 B	26-08-1993
		AU 6205490 A	07-03-1991
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		DD 297448 A	09-01-1992
		JP 3224489 A	03-10-1991
		MX 22123 A	31-01-1994
		NO 903812 A	04-03-1991
		NZ 235115 A	25-09-1991
		PT 95171 A,B	25-06-1991
WO 9534223 A	21-12-1995	AU 2669795 A	05-01-1996
		EP 0765127 A	02-04-1997
		JP 10501412 T	10-02-1998
		ZA 9504924 A	20-02-1996

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